

# **FIGURE 1**

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGTCTCCCG  
CAGCGCTACCCGCCATCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTCTGCTG  
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGCCGGCTGGGGCT  
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGCGGGAAACA  
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
CTGGAGGGCTGTGCGAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGCGCAGGAGGA  
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGCGACGGGCCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGAAACGAGACCCACAGCATTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGCTGGTGCT  
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACCGGAGGGAGCA  
CGGACAGTGTGCAAGATGTGGACGAGTGTGCTCACTAGCAGAAAAACCTGTGAGGAAAAACG  
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTCGAAGAAACG  
GAAGATGCCGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCCTAAATTATTAGAAGGATGTCC  
CGTGGAAAATGTGGCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGAGAGGCTG  
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTCTTA  
AACAGACTTGTATATTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA  
TCACAAATTTCACAAATAAGCATTTCAGCTAGTTGTGGTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAGAACCGAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCAGTC  
ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL  
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG  
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWVLDE  
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT  
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

### **FIGURE 3**

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACCGCGTCCGCCAGGCCAGGGAGGCAGCGCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGGTGC  
GCACGAGGAGTTTCCCGCAGCGAGGGAGGTCTGAGCAGCAGATGGCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGACTGCAGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGGCCTGTACCTATGGATCGATGCTCACAGGAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTTACACATGAT  
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTGGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGCCCTGTCTGGAACAGTGCCTCACAGGCA  
TCAGTTGTTCAAGTTGGTCCATGTCTGGAAAACAGGATGGGTTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT  
TCTTTAAAACATGTCAACAAGCTGAGTGCCAGGGGGTGGCAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCCACGATGTATGAATGGTGGACTTGTGTGACTCCTGGTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACGTGACAAAGCAAACGTCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTCTACCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACACCCTGTCGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAAGGGAGACCTCTGTCGAAAGCCTGTCTGCCAGCCTGGCTGGTGACAT  
GGAACCTGCCATGAAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC  
ACACGCCCTCACTAAAAAGGCCAGGAGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACGCCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTCATTACACTTAAGAATACTGCCCTGAATTATTAGCT  
TCATTATAATCACTGAGCTGATATTACTCTTCTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTCTGTTCACTGCTTGGACAGATTTATATTGTCATTGTA  
TCAGGTTAAAATTTCAGTGTGTAGTTGGCAGATATTTCAAAATTACAATGCAATTGTT  
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACGCATTCAAGATTATTGTCAGATATTAGAT  
GTTTGTACATTAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACCT  
TTACCAATTCCAGAGATTCACTGTTGGACAGATTTATATTGTCATTGTT  
AAACAAATATAATATTCTAAACACAATGAAATAGGGAAATATAATGTTAGTAACTTTGCAT  
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAACATT  
ACTGTTGTATGTAAAAATAAGGTGCTGCTTGTAGTTGGAAAAA  
AAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCGACCTGCAGAAGCTGGC  
CGCCATGGCCCAACTTGTAAATTGCAAGCTTATAATG

## **FIGURE 4**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSRLSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNNGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCCGGCGTCGAGGCCAGGAGGGGGAGGCCGGCGCGGGCCAGCCTGGG  
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGCCACTGGCTCTGGGTGCCAGCAGGGTGTGGCGCCGG  
GAGCTAGCACCGGGCTGACACTGCCGGCATCCGGACGCCGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCAGCAGCTGTGCCCTGCCCTACCTGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGACTTC  
TGCCTCGGCGTGCCACCCCCCTTTCCCCCGATCCAAGGATGTATGCATGGAGGTGTATCTA  
TCCAGTCTGGAACGTACTGGACAACGTAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGGCCCTCTGGGCATGACCCTGAGGGCATTGCCTACGCCCTGGCACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTGATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCGTCTGCGCCCAGAACCTGCTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCCGGGCTCGATGGTGCCTGGTGGTTCTGGCTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTGGGGCAAGGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAAGTCACCCGTCTACCGCCT  
CGGCCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGACTGCCCAACTCCTGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGATCGCGCGCGTCAATGAGTGCACATCGAG  
AGCTTCTGCTGGCGTCTGGGCCCGTGGCATGGAGGACATGGTCACTGAGGCTG  
CGGGCACCACGCCGGCTCCGGCTGGGATCCAGGCTAAGGGCCGGAGAGGCCCAATG  
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCAGGCCAGGGCGCTAAT  
CCCAGCGCGGGTCCGCTGACCGAGCAGGCCCTGGGAGGCCGCGGGCAGGGCAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGACGGGGCAGGGCTGGGAGAGAGCACAGCTGCAG  
ATCCCAAGGCCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATAACCCACCCCAATCCCGTATTCTTTTTTTTTAGACAGGGTCTTGTCTCCG  
TTGCCCAAGGTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA  
AGTGAACCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC  
TAATTTTGATTTTGAAAGAGGGGGTCTCACTGTTGCCAGGCTGGTTCAACT  
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA  
TAAAACCAAAAGTATTGATAAAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
```

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA  
ATTCTCTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTGGGGCAAGGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCCCTATAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCATCCGCGCAGTTGGCCTCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGG**ATG**ACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCAG**TAA**AGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCCCTGGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATCGTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPafSTLNpVLRHLPQEAfPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACCGCGTCCGAACCTCTCCAGCGGGGAGCCGCCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC  
GACCAGCTGAGCAGGCCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACCGGGCGTCGCATCTCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGGCCAGCGGAAGAGCAAAGACTG  
CGTGGTTCACGGAGATCGTGGAGAACAACTATACGGCCTCCAGAACGCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGGGCAGGGGGCCCGCCAGGCTCCCGAGCCGAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC  
CGAGAACAGAACAGCAGTTGAGTTGTGGGCTCCGCCCGGACCAAGCGCACAC  
GGCGGCCAGGCCCTCACGTCTGGGAGGCAGGGGGCAGCAGCCCTGGCCGCTCCC  
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGA  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTAGCGACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGCCAAACTCCTCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKD  
CVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHA  
EKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTGACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCATCCAGT  
CATTGGATTGCTGTTATTTTTCTTTTCTTTCCCACCACATTGTATTTAT  
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGGCCAGCCATGGGCTTTTCCT  
GAAGTCTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTCAAACCTCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACTTGTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAAATATGC  
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAAC  
AACTGGACGAATTCCCCATGAACCTCCAAGAATGTCAGAGTTCTCATTGCAGGAAAAC  
AATATTGACACCATTTCACGGGCTGCTTGCCTAGCTTGAAGAGCTGCACCT  
GGATGACAACCCATATCCACAGTGGGGTGGAAAGACGGGCCCTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTCTATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGAACCTCTGACCAACAAGGGTATGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCAAATTGTAACGTAATTGCTGTCC  
CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAGAT  
AAACCACATTCTTGTACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGATAACCCTGGTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
ATATATCCCTCATCTCAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCGTCAGGGATTAAATATGAATCTTGTCTGTCCCACCAACGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCCTCAGCCTCCACCCCTCTCTAT  
TCCAAACCTAGCAGAAGCTACACGCCTCCAACCTACCACATCGAAACTCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTTGTGAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGATGGCATA  
CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGGCATGTTAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGTAGAAGACACATTGTTAGGAG  
CACCACCCATGCCTCTATCTGAACAAACGGCAGCAACACAGCGTCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGTCTGCTCAGCGTCTTGTGGCATATGCACAAAAGGGGCGTACACCTC  
CCAGAAGTGGAAATACAACCGGGCGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCATCCTGGAGATGACAGAAACCAGTTTCAGATGTCCTCTAAATAACGAT  
CAAACCTTAAAGGAGATTTCAGACTGCAGCCATTACACCCAAATGGGGCATTAATT  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCACGCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCAGAACATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT  
TTGTCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG  
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGCTTTAAATCTT

## FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLL~~ACPSVCRCDRN~~FVY~~CNERSLTSVPLGIP  
EGTV~~VLY~~LHNNQINNAGFPAELHNVQSV~~HTVY~~LYGNQLDEFPMNL~~PKN~~VRVL~~H~~QENNIQTI  
SRAALAQLLKLEELH~~DD~~NS~~I~~STVGVEDGAFREAISL~~KLL~~FLSKNHLSSVPVGLP~~V~~DLQELR  
VDENRIAVISDMAFQNLTS~~LER~~LIVDGN~~LL~~TNK~~G~~IAEGTFS~~H~~LT~~K~~KEFSIVRN~~S~~LSH~~PP~~PD  
LPG~~THL~~IR~~LY~~LQDNQINH~~I~~PLTA~~F~~SNLRK~~L~~LD~~I~~SNNQLRMLTQGVFDNL~~S~~NLK~~Q~~LT~~A~~RNN  
PWFCDCS~~I~~KWVTEWL~~K~~Y~~I~~PSSLNVRGFM~~C~~QGPEQVRGMAVRELN~~M~~NLLSCPT~~T~~PG~~L~~PLFTP  
APSTASPTTQP~~P~~TL~~S~~IPNPSR~~S~~Y~~T~~PP~~T~~TSK~~L~~P~~T~~IPDWDGR~~R~~VT~~P~~P~~I~~SERIQL~~S~~IHF~~V~~ND  
TSIQVSWL~~S~~LF~~T~~VMAY~~K~~L~~T~~WVKM~~G~~H~~S~~L~~V~~GG~~I~~V~~Q~~ERIV~~S~~GEKQH~~L~~SLVN~~E~~R~~S~~TYR~~I~~CLV~~P~~L  
DAFNYRAVED~~T~~ICSEATTHAS~~Y~~LNNGSNTASSHEQTTSH~~M~~GSP~~F~~LLAGL~~I~~GGAV~~I~~F~~V~~L~~V~~L  
LSVFCWHMHKKGRYTSQWK~~Y~~NR~~R~~R~~K~~DDYCEAGT~~K~~K~~D~~NSILEM~~T~~TSFQIV~~S~~LNNDQ~~L~~KG  
DFRLQ~~P~~IY~~T~~PNGG~~I~~NY~~T~~D~~C~~H~~I~~P~~N~~N~~M~~RY~~C~~N~~S~~S~~V~~P~~D~~LEH~~C~~HT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## FIGURE 14

ACTTGGAGCAAGGGCGGGGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGCTCCACGAGCG  
ATCCCCGAGGAGAGCCGGCCCTCGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGCTGCGCCCTGCC  
TCGCTTCCCAGGCAGGCCGGCTGCAGCCTTGGCCCTCTGCTGCCCTGAAAATGGAAAAGATGCTGCAGGCT  
GCTTCTGCTGATCCTCGGACAGATCGCCTCCCTGCCAGGGCAGGGCGTACGTGGAGGTCCATCT  
CTAGGGCAGACACGCTCGGACCCACCCGAGACGGCCCTCTGGAGAGTCTGTGAGAACAGCGGGCAGACC  
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCITGCAATTCTTGACATTGGCTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAGAACATG  
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGCATCTGCCACGG  
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGCAGAGGGGCCGGCCCTGA  
GGGAGAATGTGCCACGGGTCTAAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCGAGGTGGCTGCTA  
AGGCACGGGACACGGGATCTTAATCTTGCCATTGGTGGCCAGGTAGACTCAACACCTGAAAGTCCATTG  
GGAGTGAGCCCCATGAGGACATGTCTCCTTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGAGCACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCGAGAATCCAGGATCTGT  
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTCTGCCAGTGCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTTGACTACTGTGCCCTAGAAAACCACGGATGTGAAC  
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCCATGAAGGATTTGCTCTAACCCAGATGAAAAAA  
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAAGCCGAGTGGACACTGTGCAC  
AGCAGGACATGGCTGTGAGCAGCTGTGTGAACACCGGAGGATCCCTCGTCTGCCAGTGCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCGGGGATTACTGCCCTGCTGAGTGCACATGGTTGTGAATACTCCT  
GTGTCACATGGACAGATCTTGTGCTGAGTGTCTGGGACACGGCATGGGAAGACGTGTG  
CAAATTGGACTCTTGTGCTGGGGACACGGTTGTGAACATTGCAAGGAAAGATGCTGTTGTGAAGGATTCGTTGTG  
GCCAGTGCTTGAAGTTATATACTCCGTGAAGATGGAAAACCTGCAAGAAGGAAAGATGCTGCCAGCTATAG  
ACCATGGCTGTGAACACATTGTGTGAACAGTGAGCAGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTGCAATCAACCCACCATGGCTGCCAACACATTGTGTTA  
ATAATTGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTCAAGAAAT  
GCACTGAAGGCCAATTGACCTGGCTTTGTGATCGATGGATCCAAGAGTCCTGGAGAAGAGAATTGGAGGTG  
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGACAATTTCCTCAAAGCCGCTCGAGTGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAGACATGAAAAAGCCGTGGCC  
ACATGAAATACATGGAAAGGGCTTATGACTGGGCTGGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG  
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTTGTCACCGACGGACGGCTCAGGATG  
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCATGGTATCACTATGTATGCTGTTGGGTAGGAAAAGCCATTG  
AGGAGGAACACTACAAGAGATTGCTCTGAGCCACAAACAAGCATCTCTTATGCCGAAGACTCAGCACAATGG  
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGAAACTGCCAAAAACGGTCAACAGCCAACAGAAATCTGAGGCCAGTCACCCATAATATCCAAGACCTACTTT  
CCTGTTCTAATTGCACTGAGAACACAGATATCTGTTGAAGAAGACAACTTACGGTCTACACAAAAGCTT  
CCCATTCAACAAAACCTTCAGGAAGGCCCTTGGAAAGAAAACAGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTCAAGAACAGAAGTAAGAAAATTAAACACAGCCTTAGAAGAAATGACACAGAGAATGGAAGGCC  
TGGAAAATGCCCTGAGATACAGATGAAGATTAGAAAATCGGCACACATTGTTAGTCATTGATCACGGATTACAAT  
GAACGCAGTGCAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTGCCACAGAACAAAGACAAGAGTATACACTAACTTGTATAAATTATCTAGGAAAAAAATCCT  
TCAGAATTCTAACAGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTGAAATATACTGTGGACAC  
AACTTGCTTCTGCCCTACCTGCCCTAGTGTGCAATCTCATTTGACTATACGATAAAAGTTGCACAGTCTTACTT  
CTGTAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTTGATATATGTATATGGATGTATG  
CATAAAATCATAGGACATATGTAATTGTGCAACAGTTGATTAAATACAATATTAAATTCACCACTTCAG

## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAEGRPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG  
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSALGDHGCE  
HSCVSSEDSFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR  
LAEDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEDNLLRSTQKLSHSTKPGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCGCCACGCTCCGCCGTCGCCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCGCCGGCTGGCGCCCTGACTCCGTCCGCCAGGGAGGGC  
**CATG**ATTCCTCCGGGGCCCTGGTACCAACTTGCTGCGGTTTTGTTCTGGGCTGA  
GTGCCCTCGGCCCTCGGGGCCAGCTGCAACTGCACTTGCCCACCGGTTGCAG  
GCGGTGGAGGGAGGGAGGTGGTCTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCTGCCGGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTAATGGTCTCCAGCTCCTCATCCTGCCGTCTCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTATCCGTG  
GGTCTTAAGCCTACCAACCTTCTGCTCTCATGGCTGGAGTCTATGTCAGGCCAC  
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAGTGGACACAGGGCTGGAGCTGC  
AGTGGTGCTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCCTGCCCTGCCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC  
TTCCTCTGTACCTCCGCACGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT  
GGGGCCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCC  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**TGATGAC**  
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTCTATAAGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC  
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGCAGCTCCAGGC  
CCCCCTGATCTGTACCCACCCCTATCTAACACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAAGGCTGGCTGGTTAGGTTTACTGGGAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTGTTCTTCAAATTAAATAAGATACATAA  
TGTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA  
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCCTCCGCTCCTAGTGGTTTTCCACTTTG  
TTGAATTGTTCTATACTCAAATTGCAACAGACACCTGTCTCCAAATGCAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTTAACAAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGTACAAGAAGTCTATAGAAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACACA  
CTATCTAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAATTGTAAAACCGTGAAT  
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTAAGGATATCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTCTTTGAT  
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGAATGTTGCAGTTGCATTTTATATTATA  
AGAGTATTGGTCTTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCTAGTCTCAATGAGCTCAAACCC  
ACCCACATTATGAACCTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATT  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATT  
ACCTCTGGTCTTCAGTCAAAGCACCAGGACAACAATTCAAACAAATTCTTGTG  
TAGCCTATTCTTGCTGAACCTGTTCTTGTGGATCAATACAAACTAATAAGCTCT  
TCTGTTCAATCATTGCCGGACTGCTACACTACTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATT  
CAAGAATTATTATCTTGCTATCTAACGCCAGCCGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCAGAAACAACTTATT  
TGGAGTTTATAGGACCAGCATGCCATTCTGTTAATCTCTTGGCTTTGGAGTCAT  
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGGAGAACA  
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTCTGGCCTTCGGCACCACCTGGATCTT  
GGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACACTTCACAGTCAGCAATGC  
TTTCCAGGGATGTTCAATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT  
ATTACAGATTGTTCAAATGCCCCCTGTTGGATTTAAGGTAAACATAGAGAATG  
GTGGATAATTACAACGTGCAACAAATTCCAAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTCCAATTAACTACTAGACAAAAAGTATTAAATCAGTT  
GTTTATGCTATAGGAACGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT  
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA  
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC  
CCTACCACCTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA  
ATATCAAACAGTGAAAAGGAATGATAAGATGTATTGAAATGAACATGTTTCTGTAGAC  
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCACTTGTGAA  
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTGTTGCTAAATCTGTTCTT  
TTCTAAATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 19**

MKRLPLVVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTESYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCAA  
NINKLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTFVKTVNNFVQRDTFVWDKLSVNHRTHLTKLMTVEQATLRIQSFKTTEFDT  
NSTDIALKVFVFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAIICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSIAGL  
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSaalgyryygt  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVILHVVASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACCTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC  
TGGTTCTCAGTGAAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCCGGTGGGAGGAGTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTACCCCGGCTGGGA  
CAAGAAGCCGCCGCTGCCCTGCCCGGGCCGGAGGGGGCTGGGGCTGGGCCGGAGGCAG  
GGTGTGAGTGGGTGTGCGGGGGCGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG  
CCGCGCGCCGTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCAAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGTCGCCGCCAGCCTCCGCACCCCATCGCCGG  
AGCTGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGCCCTCTGGCTGGCCGTGGCCGGCGCCCTCGCCTCTCGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCACCCCATCCGCTGCCGCACCTGTACACCTCCGGCCCC  
ACGGGCTCTCCAGCTGCTTCCCTGCCATCCGTGCCGACGGCGTGTGGACTGCCGCGGGG  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTGCCGACGGCAAGATGCAGGGCTGCTCAGT  
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCAGGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
ACTCGGAGGAAGACTGTGCTTCTGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACGCCCTCCGGCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCATTTCTGCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCCAGCTTGAGAAGTAACT  
GAGACCATGCCCGGCCCTTCACTGCTGCCAGGGCTGGTACCTGCAGCGTGGGGACG  
TGCTCTACAAGAACAGCTCTGAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAAGAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT  
CATACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCCATCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGACTGTCTCAGTTCTGCTGAATACTCCATCGATGGGGAAC  
TCACTTCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCAGGG  
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCACCAG  
GCTTCAGGAGTAGGGGAAGCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCGGTGTACCTGC  
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCCTATGTCAACCTGCACCTCTGTTCAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCAAGTCTGTCAATAACTGCTGTGGAAGCAGGGGGAAAGACCTAGAAC  
CCTTCCCCAGCACTTGGTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTCTTACATTATTATGCCCAAATTATTTATGTATGTAAGTGAGGTTG  
TTTGTATATTAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAACGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGAGGAGGAGCCACCGCCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTCCCTCCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCCAGCAGTT  
AGCAAGGCCAAACCTGGAAGAGGATACTGACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCGTGAAGCCGCAATT  
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTGAATGTGCAGTGGCTACGCCTGTAATCCCAGCAGTTGGAGG  
CCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA  
AATAAAATAGCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD GIRLLENPRILGSQST  
NSSYT MNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRC PGKRMQVDDLNISGIIIAAVVVA  
LVISVCGLGV CYAQRKGYFSKETSFQKSNSSKATTMSENVQWLTPVIPALWKA AAGGSRGQEF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCCACAGCCGGACCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTACATACACTCCACCTCAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTCTCTTCTCCAATATGCATGACATTGGACAATG  
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTCTATGGCATTCA  
TTGACAAATGCAAGCATCTTCTTATCAATCAGCTCATTGAACTTACTGACTGACTG  
TGGAACTCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCACTGTGCTACTTGGCTAGCTACACTACACTAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGTACGTGAAATCAGGCTTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATTGAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTAAACAAATTATCTCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCTCGACTGAGCAACTAACAGACTATTAATCACA  
ACTGCCTGAAAATGCTGTGCGACTGAGCAACTAACAGACTATTAATCACA  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC  
AATTCAAATAGATTGAGATGATCAACAGTAAGTGGTTGATGCTCTCCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTATCA  
ATCTTCGAGCCTGGTTAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTGGTT  
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT  
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCTTATTAGAA  
TACGAAGGGGTGATTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATAATAGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTACATTACCCCAATGCATTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCAGTGCCTGTACCATGGTACCATGAGTCTG  
CCAAACCTCAAGGAATCAGCATAACACAGTAACCCATCAGGTGTGACTGTGTCATCGTTG  
GATGAACATGAACAAAACCAACATTGATTGATGGAGCCAGATTCACTGTTTGCCTGGACC  
CACCTGAATTCCAAGGTCAAGATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG  
CTCCCTCTTATAGCTCTGAGAGCTTCTCTAATCTAAATGTAAGCTGGAGCTATGT  
TTCCCTTCAGTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA  
GATATAATGGCGTAACTCCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTGAAAGTCTGTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG  
GCTCTTGAATATTAAAATAAGAGATACTCAGGCCAATTCAAGTTGGTGTCAAGACTGAAAATTCTCA  
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA  
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTATGGCCTGTCTGGAGGCCTTCTGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTGATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCC  
AAAAACCAAGGAAACCTACTCCAAAATGAAC

## FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKTELPEKCLSELNLQELYINHNLLSTISPGAFIGLHNLRLHLSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRLSIVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNLKFLLDNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVT KGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENNCDGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC  
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTATGCTGACATTCCAGC**ATGAATCT**  
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTTAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAATGCCCTCAATAACCTGAAGGCCAGGGCCAGAATTCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCCTCAATGCTGC  
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTGGCTGGTCACTATGGTATCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGT**A**TAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTGAA  
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTT  
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATTGGGAAAAAAAAAAAAAAACA

## FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNICKTSVLDEHAGRFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVVISYVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGAACGAAGGCGGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGTCTTGAGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAACCGCTCAACCAGGACGAGTTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCGTGGAGGCCGGCG  
CCTTCAACAAACCTCTCAACCTCGGACGCTGGGTCTCCGAGCAACCGCTGAAGCTCATC  
CCGCTAGGCGTCTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGGCCCTAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT  
CATCGCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTGGACACCATGACACCCAAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCGTCCGCCACCTAGTCTATCTCCGTTCCCTCAACCTCTCCTACAACCCATCA  
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGAGCTGGCGTGGTGGAGCCCTATGCCTTCCGCCCTCAACTACCTGCGCTGCTCAA  
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCGCTGGCCTGCAGTGTGGCTCCTGTGGTGTCCGG  
CGCCGCTGGCGCTCAACTTCAACCGGAGCAGCCCACGTGCGCCACGCCAGTTGTCCA  
GGGAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACACGGTGCAGTT  
GTGTGCCGGCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGGGCCAACGCCGGCAACGAC  
TCCATGCCGCCAACCTGCATGTGCGCAGCTACTGCCGACTGGCCCCATGCCAACAA  
GACCTTCGCTTTCATCTCAACCAGCCGGCGAGGGAGAGGCCAACAGCACCGGCCACTG  
TGCCTTCCCTTCGACATCAAGACCTCATCATGCCACCCATGGCTTCATCTTT  
CTGGCGTGTCTCTTGCTGGCTGCTGTTCTCTGGAGCCGGCAAGGGCAACAC  
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTGGACGCAGGCATCAGCTCCGCC  
ACGCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGCGGGGGCAGGGACCCCG  
GGCGGCCGGGAGGGGAAGGGCCTGGCGCCACCTGCTCACTCTCCAGTCTCCCACCTC  
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGTCCCTGCTGCCCG  
CCAGCCCTCACCAACCTGCCCTCTTCTACCGACCTCAGAACGCCAGACCTGGGACCCCA  
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATTTT  
TATGAAAACCTGAAATAATAAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDQDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSIHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMIHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCCACGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGCGCCCAGCC  
AGGGAGCCGCCGGGAAGCGCG**AT**GGGGGCCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
TGTCGCCTGCTGGCGCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCCCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCACTGGTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTCTAGGAATTCCACAGAACGCCATCATCACTGGTT  
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCACTTCTGGGAGCAAG  
CCTGCAGCCGGCTCACCTGGAGAAAGGGTACCAAGAACCTCCACGGAGAACCAACCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCACTGGTACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTCCCTTCCTCAACAAAGAGTGCACAGTGGCACCTACGGCTGCACAGCCACCA  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGATCGTGGCTTCATTGTCTCCTGCTG  
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCACT**TAG**AGGGCCCTGCCACTTCCTGC  
GCCCCCAAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC  
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGGAGCCCTGGGTGAGAAAAGCAAAAACA  
AACAAAAAACA

## **FIGURE 32**

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCSIFTMPVRTAKSLV  
TVLGIIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTCTTGTGTTGCCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCATTTATTCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTTCGCTAACCTTATAATGCCGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG  
CTGCACATCAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG  
ACTTGAACAAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGGAGATCCTGCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTGGAAAAAACGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCAACCTCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC  
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCATCCCAGGGTGGTTAAAGATGAAC  
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAATCGACTTGTGGATTACAAGA  
ACCTCATTCTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACTG  
CTGAGGTCCCTGCCTGGACGTGTTGCTGGGGCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCGAGTTAACCTCCATCATCCAGA  
TAGACCTCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCTTCAAGCAGTGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT  
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCCACGTTAACTTGCACAGTAAACAGCACTGGGTTGGCGAGACCAGGACGCACTCC  
AACTCCTACCTAGACACCAAGCAGGGTGTCCATCTCGTGTGGTCCGGGACTGCTGCTGGT  
GTTTGTACCTCCGCCCTCACCGTGGTGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGAGCAGAGATGCCAACCTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTG  
GACTCTCCTACTGGACAATGGGCCTTACAACCGAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG  
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTGCACAACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTTGTGAGAGCCCTTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG  
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCGTGGGGTTGGATGCCGGTTCTATAC  
ATATATAACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNKI  
KSFRQK TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLI  
LNDNLISTLPANVFQYVPITHLDLRG  
NRLKTL PYEEVLEQI PGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSL PAPPAQEETFAPGPLPTPFKTNQEDHATPGSAPNGGT  
KIPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCNNRN  
VSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYN  
AIQLILPGTFNAMPKLRILILNNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEV  
LMSDLKC  
ETPVNFFRKDFM  
LLSDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLL  
VFVTS  
AFTVV  
GMLV  
FILRNR  
KRSKRR  
DANSS  
ASEINS  
LQTV  
CDSSY  
WHNG  
PYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTGTGCGGCCATAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGATTCTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGGAGGG  
AAGGGAGGGGAAACGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG  
**AGAATGAGGCCGGCGTTGCCCTGTGCCTCCTGGCAGCGCTCTGGCCGGCCGGCGG**  
CGGCGAACACCCCCTGCGACCGTGCTGGCTCGGCCTCGGGCCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCCGGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCAGGCCGGAGCTGCAGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG  
GCCCGGAGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCCTTCCACT  
GCACCCCTGGAGAACGAGCCTTGCAGGGGTTCTCTGGCTGTCTCCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGGAGGAGGCCAACGCTCCTGCACCGCGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGGCCGAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTGTGCTGCGCCGCCCCGG  
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGGCCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCTCCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCCAGAGCTCCCTAATGCCTAGACGACTTGGGAGG  
CTTGCCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCGCTTGTGACCA  
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGTGCCCACCAGCGCCGCCACT  
GCAACCAGCCCCGTGCCAGAGAACATGGCAATCAGGTCGACGGAGACTGGGAGAGAC  
ACCACCTGTCCCTGAACAAGACAATTCACTGAAACATCTATTCCCTGAGATTCCCTGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAAATGTCCCTCAAGCCGAGTCAGGCAACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCCTCTGCCACTCCCTCAGGCTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTCAAGAACGCCCTTCCAGCCA  
AGGAAGGAGTCTATGGGCCGCCGGCCTGGAGAGTGATCCTGAGGCCGCTGTTGGCTC  
CAGTTCTGCACATTGCACAAACAAATGGGGTGAAGAGTGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTGCTGGGGAGTCCCTCTTGCTCTAGTGATGCATAGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACAGGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTGACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTCTATGTTATTGGAGAA  
TTTGGAGAAGTGATTGAACCTTCAAGACATTGGAAACAAATAGAACACAATATAATTACA  
TTAAAAAATAATTCTACCAAAATGGAAAGGAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDILFWVALERRSHTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## **FIGURE 37**

CGGACGGCTGGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATGCCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC  
CCCCGGCTACCTGGGCCGCCCGCGCGGTGCGCGTGTGAGAGGGAGCGCGCGGGCAGCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCCGTGTGAGCGCGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCTGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGGAAAATCA  
CAGTCCCAGGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGCCAGCGCATTGCCG  
CTTCTGTGGACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC  
CCCCAACTGGCCAGACGGGATTACCCCTGCAGGAGTCACTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGCCGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTCTTATTCA  
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTAGGCCAAA  
AAACTGCCCTACAACACTACAGAACAGCCTGTCACCACACATTCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCCTTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTGTATTAGCCGGACTGTTATCACAAACCATCACTCGCGATGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGGCCGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAACAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATAGAACGCTCTGGATGCCCTAAAAATAAGCAATG  
TTAACACTGAACGTGTCCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT  
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATCCGAAAGATGG  
GAAGTGGTTGACTCTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTCAAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCAGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTATACATCTGTAAAAGGAT  
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTAGAAGTGCATATTATAGT  
GTTATTGTTCACCTCAAGCCTTGCCCTGAGGTGTTACAATCTGTCTGCCGTTCTA  
AATCAATGCTTAATAAAATTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQOSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESDNLCRYDFDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMQVGVEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTACACTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACATCCGGGACAACACTTGGAG  
GTGGAAACACTGCCTGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGTATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA  
GTGGAGCTGACCAATTCTCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA  
ACAAGCAGTGTAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGCCA  
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGA  
TCGCGGCCACCACTGTAGGACCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCCAGTTCTGT  
TCTGTGTTACCCACATCCCCACACCCATTGCCACTTATTATTCAGGAAATAAGA  
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPKGLVPAVLWGLSLFLNLPPIWLQPSPPPQSSPPPQPHPCHTCRLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPCCPGTERPCGGYGCCEGEGRGGSGHCDCQAG  
YGGAEACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAKGDLVFTAIFIGAVAAMTGYWLRSERSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCTGGCTCTGCTGGCACTCTGGGTGTTGCCAGCCCCGGG  
GCCGCCCTGACGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTCAGCTAAAGAGGT  
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTATCCCCACCCACGTGAGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCGTCTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGGCTGTCCCCCGCAGCGCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCGCTGGCGTCCGGCCACAAGCTGGTCCGCTTGCCTCGCAGGGGGC  
GCCAGCCGGCTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCCGGCTT  
CCTGGCTTATGAGTGTGGGACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTCTGGGCCTCGACAGTCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTAGGCATAGGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCGAGAGCTG  
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTGGCTTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTCTATTCTTATTCACTGCACTATATTCTAACGACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTGTCCTGTCAC  
TGGATCTGGCTAAAGTCCTCCACCACCTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVPIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRILPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWP  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGGCGGCTGTTGTCACTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTCTCCCGTGTGGAGTGGAAAGTTGACCA  
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG  
TGACCTTCTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCTCCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTTCCCCACCTCTGAATAACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTCCTATGTCCT  
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTTGTAAACCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCTTACT  
CAGGTGCTACCGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCTTATTGTCCT  
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAAGTAGACAGCAAAATGGCGGGGGTCGCAAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATTTGAATAGGTATCTTGAGCTTGGTCTGGCTTTCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGGTGG  
TGATGACACTGGGGCCTTCCATCTCTGGGGCCACTCTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTCTGCCCTGCTCCTGAATAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTTGAAGCCAAAAG  
GATTAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTCACGCC  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGAGTCGGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELEVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNFGVIVAAVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCCGCTGTGGGGACAGCATGAGCGGCGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTGCCACCCACCAAGTCCAGTGCAGCACCAGTGGCTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCACCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCATGGGTTATTGAGCTGCTGCCGTGC  
TCAGTGCAAGCCTGGTACCGCCACCCCTCCCTTTGTCCCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC  
CTCGCTGCCCTGAGGACAAGCAACTGCCACCCAGTCACCCAGGAGTGTGAGTTCTT  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCGAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLDCCSDGSDEEECRIEPCIQKGQCPPPGLPCPCTGVSDCSGGTDKKL  
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGGCAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGAGGAGGAGGAAGGAAGGAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTAGCTGGCGTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA  
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTCTTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAA  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAAACATCTGTGAGC  
TCCAGACCTCCTTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCAATGGTAGTCACGGAGATTCGTCT  
GCCACCCGGCCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCT  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGGCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG  
ACGAAGCTGTGAGTGGCGGTTGAGTGCCTTAGGCCCCGGTACATGGCTCTGTGGCCAG  
GGCTGCCCTTACCCGTGGACCGACAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCACCCCTGCTGGACAACCTGACATA  
ATTGCCAGCAGGAGGGAGGTGGCATCCACCAGGCCAGGCATCCATCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGGTTAGACAAATGTAACAA  
AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC  
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACACGCGTCCGCTCCGCGCCCTCCCCCCCCTCGCTCGGGTCCGTCGGTGGCCTAGAGA  
TGCTGCTGCCGCCGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGGCCGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGGTGGGCTGCCGCCGACGGGTCGCCTGCTGAGTGCC  
TCGGATTGGAACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCAAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAAATGATAGAA  
AAGTTCATTGAAAACCTCTTGCACATCTGATGGTGAACCTCTGGATTGGCTCAGGAGGCAGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT  
CACAATTTAGGAACCTGGTATGTGGATGAGCCGTCCTGCCAGCGAGGTCTGGTGGTCA  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAATTCATTTGCAAATATTCTGATGAGAACACCAGCAGTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAACAGAACACAG  
GAAGAACATGCCAAAAAAACATTAAAGAAAGTAGAGAACGCTGCCTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCTCTCCTCCTCTGTGGTCAACCACAGTGTATGTTGGTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTCACCAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAACATTCTGAGTGTGTT  
CGGGAGAACCCACTCCGATGACATGTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAATGAAACTGACAACAATGAAAAGAACATGATAAGCAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAAACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTTGCACAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACTTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTCTGCTCTATACAG  
CAGCACATATTATCATACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAGA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPyMFQWNDDRCNMKNFICKY  
SDEKPAVPSREAEGEETELTPVLPPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLL  
VTTVVCWVWICRKRKREQPDPSKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSCGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFS  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT  
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCA**ATGATCACTGGTGT**  
GTTCAGCATGCCTGTGGACCCAGTGGCGTCCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTGTTGACACGGGGCTGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT  
GCAGCAAATGTTGCCTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGGAACCTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGAAATGAAGAG**TAAC**TGATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAAACCTAAATATTGCTGCTTGGGACCTCCTCTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTGACCAAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAACAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA  
GCACCCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA  
GGATTGCCCTCTGGCCTTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCA  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACAACCTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGGGAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCACAGATTGGGGTTACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGCTGCCCTGATTCTCAGGCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAACACTACATCA  
CCACCTTCCTATGTCCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA  
CACCAATTGTCCTGTTCTGAAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC  
TATGTGTTAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDWTWECEDPFDLRLVG  
GDNLCGSRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC  
CCACCGCGTCCGCGGACCGTGGCGGACCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACACAGGCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGTCACAAAGTGGG  
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAAAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGTTATTGCAGCTTATAATGGTTAC

## FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPVLVTFDLTDGAIVAAAEEILQCFGYVDIL  
VNNAGISYRGTIMDTTDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTIAPGLFFSLMASRARKERKSKNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

## **FIGURE 58**

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## **FIGURE 59**

CCCACCGCGTCCGGAGCGCTGGTCGACTAGTTCTAGATCGCGAGCGGGCCGCCCGCGCT  
AGGGAGGAGCACCAGCTCGCCGCACCCCTGAGAGATGGTTGGTGCCTAGTGGAAAGGTGATTG  
TTTCGCTGGTCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTCGCTCCCTATAAGAAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTT  
TTCCAGCTCAGATAACAGCCAGAAGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGG  
AGGTTCATCCATGTTGACTCTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCACTGAGGACGATGT  
AGCACGGGATTATACAGTGCACTAATTCACTTTCCAGATATTCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGGAGTCTTATGCAAGGAAATATGTGCCAGCATTGCACACCTC  
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGTATTGGAGA  
TGGATATTCTGATCCCAGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTGATGAGAAAGCAAAAAAGTACTTCCAGAAGCAGTGCCTAGTGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTGAGGCCTTGAATACTGGATAAACTACTAGATGGCAGCTAAC  
AAAGTGAATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACCTTTGCGGT  
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA  
AGATAACGTACAGTCAGTTAACGCACTGGTTAAGCTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTCACCTATGACCAGCCTGAGAGCTTGACATGATTAATCGA  
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGAAAACTACCTCCAAAAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTTGAAACAAGTGGC  
TTTGTGTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAAATTACA  
TTATTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTTAGGGTCTGAAATAGGAAGTTAATTCTTAAGAGTAAGTGAAGTGCAGTTG  
TAACAAACAAAGCTGAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT  
GTTTGAAATATTATTGATAAGAATAGCTCAATTATCCAAAATAATGGATGAAGCTATAA  
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAGTAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGREL  
VGPFPGNLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTNSNMTLRDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAAAALTERSLMGMDWKGSQEYKKAEKVVWKIFKSDSEVAGYIRO  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## **FIGURE 61**

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGAATCCCAGTCTTGGCTAACACAT  
TTTCCCTTCTAACAAAGTCTAACAGCTGTTAACAGCTAGTGTACAGGGTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGACTCTCACTCAGGGTACAGCTCCCTG  
CCTCTGTGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCCTAACATCAAATTGACTGGCTGGG  
TGAACCTAACAGCCTTTAACCTCTGGAGATGAAAAGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTGTAAAATAAATTAAAAAGCAAGTATTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAAGAGGAGACTCACAGAGCTAACACCAGGATGGGACCCCTGGGTC  
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCCTCTGCCTTGTGTTT  
GCAGAACATGTGAGGGCCAACCGGGAGGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCGCTCTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCCTCAGTCAGCACCTTCACTCTGAGAATCGTACTGGACCTCAACCAACTTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAACAGACAGGGCAGAAGAGGACAACAAGTCTCGTACCCG  
CCCCCATCGTCAGCCCTGCAGCGAAGTGTCTACCCCTACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTTACCAAGGGTCTGCA  
AGCTGCTCGGGCTGGATGACCTTCACTCTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCAGTGTCAACAAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCGACCCCTGTCCA  
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGTACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTACTGTCCAGCCGAGA  
CCCCCTGAGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGCG  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTCGCTGCACCCGGC  
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGGCAAGCCTGGGACTCACTGGCC  
AGGCCTTCAATATCACCAGCAGGACATGACTCTGCCCTGTGTGCCCTCCATCCGGCCATCAACTT  
CACTGAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCCTACGTTACAACGGCTACAGCGTGGTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTCAGATGCTCAATGCC  
ATTCAACCTCCTCAGCAAAGAGTCCCTTGGAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAAGAAGGGTTAATTGTG  
ACTTAGCTCTAGCTACTTCCCTCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLAGSL  
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAFCPIRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GGACTGGAGTGGAAACC CGGGTCCCCCGCGCTTAGAGAACACGGCGATGACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGACTCTGCTGCTGGTCTTGGGCTTCTGGTGCCTCC  
GCAGGCTGACTGGAGCACCTGGTCCCTCTGCGGCTCCGCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGGCTCCACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGACCGCCCTGCTGAAGATGAAGGCTGTGGCTTGAACACCCCTCACACCTATGTTCCGTGGAAACCTGCATG  
AGCCAGAAAGAGCAAATTGACTCTCTGGAAACCTGGACCTGGAGGCCCTCGTCTGATGCCGCAGAGATCG  
GGCTGTGGGTGATTCTCGCTCAGGCCCTACATCTGCAGTGGAGATGGACCTGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAACAGCTGGACCTTATTGACCACC  
TGATGTCCAGGGTGGTGCCTACCCAGTACAAGCGTGGGGACCTATCGCCGTGCAGGTGGAGAATGAATATG  
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGGAACACTGC  
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGATTGTCAGGGAGTCTTGGCCACCATCAACTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTCTTCACGTCAGGGGACTCAGGCCAACAGATGGTATGGAGT  
ACTGGACGGGTGGTTGACTCGTGGGGAGGCCCTACAATATCTGGATTCTCTGAGGTTTGGAAAACCGTGT  
CTGCCATTGTGGACGCCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACCTTGGCTTCATGAATG  
GAGCCATGCACTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAACCGGGCG  
ATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCCACCTG  
ACCTCTCCCAAGATGCCGTAGGCCCTAACGCCAGTCTGTACCTGTCTGTGGAGGCCCTCAAGTACC  
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG  
TGTGGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAATCTCAAGAATCTAGCCTGGATATGAAGAAGA  
GCTTCTTCAGAGGTTGCCGCTGGACAAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTGG  
GTAGCTTGTCCATCAGCTCACGCCCTGTGACACCTTCTGAAGCTGGAGGCCAGAACGCTTACCTCCAGGTCCGGTTGA  
TCAATGGCCAGAACCTGGACGTTACTGGAAACATTGGACCTGGAGGAGACGCTTACAGTTACGGAAACCCCCC  
GCAGCGGAATCAACAGGTATCGTTTGGAGGAGACGATGCCGCCCTGCATTACAGTTACGGAAACCCCCC  
ACCTGGCAGGAACAGTACATTAAGTGAGCGGTGGCACCCCTCTGCTGGTGCAGTGGGAGACTGCGCCTC  
CTCTTGACCTGAAGCTGGCTGCTGCCAACCCCTACTGCAAAGCATCTCTTAAGTAGCAACCTCAGGG  
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC  
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTCTGTGCGCAGGCTGTGGCTGTCTAGGGGGAGC  
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGCAGAACCGTGCCTGGCACCAGTCACAGCCC  
TGCAGCATCTGCTGGACTCAGCGTGTCTTGTGGTCTGGGAGGCTTGGCACATCCCTCATGGCCCCAT  
TTTATCCCCGAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTGT  
CTTCCCTCACAAACCTCTGAGCCTTCTGGGATTCTGGAGGAACCTGGCGTGGAGAACATGTGACTTCCCTT  
TCCCTCCACTCGCTGCTCCCACAGGGTACAGGCTGGAGAAAACAGAACCTCACCCCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTGGTGTCTAGTGGAGGAGACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCC  
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGG  
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGGAGGAGG  
ACAGAACGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGCAGAGCAGGCCCTCC  
GAAGTGTGTCCAAGTCCGATTTGAGCCTTGTCTGGGGCCAGCCAAACACCTGGCTTGGGCTACTGTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRR PARTLGLLLL VVLGFLVLRRL DWSTLVPLRLRHRQLGLQAKGWNFM LEDSTFW  
IFGGSIHYFRVPREYWRDRLLKMKA CGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLMMSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIV ELLLTSNDKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGWFDSWGGPHNILDSS EVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNQSFYI LY  
TSITSSGILSGHVHD RGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVRLRILVENRG RVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQK TLYLPGPWLS SGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## **FIGURE 65**

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGGTGGACGGTCCCAGGACC  
CTGGTGGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTGGCCCAGGCCCGAGGACCTCCATCTCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCGCCCCGAGGACCTCAAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCTGCCTCGTCCCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTCGTTGCTAGTGGATAGGGTCATGACCGGTTCTCTAGACGGGGCC  
CGTTCCGCTATGTGTCGGCAGCCTGCACTACTTCGGGTACCGCGGGTGTGTTGGGCCAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTAACGCCATACAGTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGCAAGG  
TGGGAGATGGGGGTCTCCATCCTGGTTGCTCGAAAACCTGAAATTCTAAGAACCTC  
AGATCCAGACTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC  
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTGGCTGGCTCTCCGTGCACTGCTAGG  
AGAAAAGATCTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCGGG  
GACTCTATACCAGTGTAGATTTGGCCAGCTGACAACATGACCAAAATCTTACCTGCTT  
CGGAAGTATGAACCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT  
CTGGGCCAGAATCACTCCACACGGTCTGTCAGCTGTAACCAAGGACTAGAGAACATGC  
TCAAGTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTGCCATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGACCCCACACCTAACGTTTGCTCTCGAGATGTACAGCAAGT  
TCCAGGAAGTCCCTTGGAACCTTACCTCCCCGAGCCCCAAGATGATGCTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTGCTTGGCCCCGTGGCCCAT  
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC  
CATGACCGTGCTATGTGATGGTGGATGGGGTGTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGAGAACATGG  
GGAGGCTCAGCTTGGGTCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG  
GGCAAACAATCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG  
GTGGTTCCCTCCAGTGTCCAAATGGCATATCTCAAGCTCTGTTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCAAGTGTGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGCC  
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATT  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAGA  
CCAGCCTGGCCAACATGGTAAACCCCCGCTCCACTAAAAAATACAAAAAATTAGCCGGCGTG  
ATGGTGGGACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAAATCC  
AGGAGGCAGAGGTTGAGTGTGAGTGGAGGTTGACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLQADTRSFVVDRGHDRFILLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAADVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGNSSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQKQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT  
CTTCGAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATTCCAGATGTCAAAACGATT  
GCGTTCCCTCTTACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCGATGCTGCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGA  
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCCTGGGTGTATTGCT  
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACCTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCTAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAATTACAGGAACGGAT  
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTTAAACGACT  
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA  
AAAACCTGGAGTCACTTTATTCTCTAACACAAGCTCGAACCTTACCAAGTGGCAGTATT  
AGTTACAGAAAATCAGATGCTTAGATGTGAGCTACAACAATTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAAGATCACCTTTGATAACCTGCCACTCGAAGTCAGGAACTGAATCAAGACATA  
AATATTCCCTTGCAAATGGATTAAAACTAAGATAATATGCACTGAGTGTGCAGGAAC  
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTGTAGGGTTAAAGTCATTCAACATTCCAAATCATTGTTCTTTAAATTGTTG  
AAAGGAAAGGAAAATTATAATCAACTAATCTGGTTCTTTAAATTGTTGAACTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLIQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLQELRHLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS  
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRLCDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSPL  
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## **FIGURE 69**

CCACACGGCTCCGGCCTCTCTGGACATTGCATTCCATTCTTTTCAATTGACAAACTGACTTTTTATTCT  
TTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT  
CTGTGTTGGGTTCTTCTCCTCCCTGACATTGCATTGCTTAGTGGTTGTGGGGAGGGAGACCACGTGG  
GCTCAGTGCCTGCTGCACTTATCTGCCTAGGTACATGAAGTCTTTGACCTCATACTGATTATGCCTGTC  
ATCGCTGGTGGTATCTGGGCCCTGCTCCTGCTGATAGTGTGCTGCTGTCTTACTTCAAAATACACAAC  
GCGCTAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGAAAAATCACAACCCAGACAAGGTTGGTGGGCCAAG  
AACAGCCAGGCCAAACCAATTGCCACGGAGCTGTGCTGCCCTGAGTGCTGTGAAGGATATAGAATGTGCCCC  
AGTTTGATTCCCTGCCACCTTGCTGTCGACATAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCTCAAA  
GCAGAGGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGAGGCCACAGAAGAAAGGCACAG  
CTCCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGCTGATAAACCAAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGGAACGTACGTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCCTTAAGGCTGCCAGCGCCTGCAAATGGAGCTGTA  
AGAAGGCTCATGCCATTGACCCCTTTAATTCTCTCTGTTGGCGGAGCTGACAATGGCGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCTATGGCAGAGACCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTTTCTATGTCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTCAAAGATTAAAGTCTTGACGGAACCTCCAGCAATGGCCTGCTAGGG  
CAAGTCTGAGTAAAAGCACTATGTTCTGTATTGAAATCATCATCCAGTACATTGACGTTCAAATAGTTACT  
GAECTAGCAAGAATTCAAAGAACTGTTCTGTCTTCACTACTTCTCTCTCTAAACATCTCTATTCCAAACTGTT  
GGCGGTTACCTGGATACCTGGAGGATCCTCACCGGCCAATTACCCAAAGCCGATCCTGAGGCTGGCTTAT  
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTTCAAAGAGATTTCCTAGAAATAGAC  
AAACAGTCAAATTGATTCTTGCCATCTATGATGGCCCTCCACCAACTCTGGCCTGATGGACAAGTCTGT  
GGCGGTGACTCCCACCTCGAATCGTCATCAAACACTCTGACTGTCGTGTTCTACAGATTATGCCAATTCT  
TACCGGGGATTCTGCTTCTCACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACCTGCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACCTAACTCTAATGGGATAACTTGCAACTAAA  
GACCCAACTTGCAAGACAAAATTATCAAATGTTGGAATTCTGCTCTTAAATGGATGTGGTACAATCAGA  
AAGGTTAGAAGATCAGTCATTACTCACCAATATAATCACCTTCTGCATCCTCAACTCTGAAGTGTACCC  
CGTCAGAAACAACCTCAGATTATTGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATAACA  
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATAAACACCCAGCATGGCTCTTTGAATCCAATTCA  
TTGAAAAGACTATACTTGAAATCACCATTATGTTGGAACCAAACCTTTGTTCAAGTTAGTCTGCAC  
ACCTCAGATCCAAATTGGTGGTCTTGATACCTGTAGAGCCTCTCCACCTGACTTTGCATCTCAACC  
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGAACACTATGGGAGA  
TTCCAGTTAATGCCCTAAATTCTTGAGAAGTATGAGCTGTGTATCTGAGTGTAAAGTTGATATGTGAT  
AGCAGTGACCACAGTCGCTGCAATCAAGGTTGTCTCCAGAAGCAAACGAGACATTCTCATATAATGG  
AAAACAGATTCCATCATAGGACCCATTGCTGTGAAAGGGATGAGTGCAGTGCATCTGTTCTCATGGTTCTAGCTCTG  
GAAACACATGCGGAAGAAACTCCAAACCCAGCCTTCAACAGTGTGCACTCTGTTCTCATGGTTCTAGCTCTG  
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGCAGACTACAAATACCAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTGAAATAATGAGGAAGGGCTGAAAGTGAACACACAGGCCATGTA

## **FIGURE 70**

MELVRRLMPLTLIISCLAEITMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDITLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFAASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVRSRKRDISSYKWKTDIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGGCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGC  
TGCTGCCGCCGCCCGTGCCTGCCACAGGCCACGCCCTCGACCCCACCTGGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTCCTCGTGCCTCGCTAGCGAGTGGTTCTGGTGGTATTGGAAAAGGAAA  
AGATAACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTAGTTCAAATATGAAGAT  
TTTGGACCACTATTTACAGCAAATTTTAATGCCAACAGTGGCAGATATTTCAAGGC  
CTCTGGTGCCTAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT  
CAGAATATTCTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCTTGGACTGTACTATTCCCTTTGA  
ATGGTTTCACTCGCTTCTGAGGATGAATCCAGTTCAATTCCATAAGCGGCAATTCCAG  
TTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTACGGAGGGACCCGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGTATAACCAGGACATCTTGCCTA  
CATAAATGGGAAAAGTCATGACAATAGACAAACTGCTGGGCTATAGGAGGGAAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTGTG  
GAGGAAATCTTTGATGAATATTGGGCCAACACTAGATGGCACCAATTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTCTAAATGGCCCACATCAGGACAGCTGTCCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCATGGACAGCCACTTAACG  
GATTCTTGAGGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACATTCAAGGATGC  
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACACTGGATAAGAAAATTATTGGCAGTTGCCCTTCCCTTTCCACTA  
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAAGTAAATTATGGTGAAGCCATATCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATAATGGTGCACCTGTATAGGGCACTTACCGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTTCAATTATAACATAAGTGTACTGTAACATTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTTAGCTAAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACG**AT****GGCC**CAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTGCCTGCAGAAGAGCT  
TTCCATCCAGGTGTATGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCAGAACCGC  
AGCTGAATTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA  
TGGATTCTGTGGTCATCTTAGGATTAGCCAAACCCAAAGTGTGGAAAAATGGGTTGGGTG  
TCCTGATTGAAAGGTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT  
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAGAAATTATTGTCAAGTACAGTACCTACTCGGTGGCATCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTCAAGAAGTTTATGAAACTAGCACCATGTCTACAGAAC  
TGAACCATTGTTGAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC  
TATGTCAAAAGGTATGTGAAGGCCCTCCCTTTACAAACAAGAATCAGCAGAAGGAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGCATGCCGAA  
GCTGAAGTT**AG****AT**GAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAACAGTCCACCCCTT  
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAGCTCCACGGCC  
TTCTAGCCTGGCTATGCTTAATAATATCCCCTGAGGAGAAAGGAGTTTGCAAAGTCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCAGTACGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGCTCTTGAGCCGGTA  
AGAGCAAAGAATGGCAGAAAAGTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT  
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAAATTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCT  
GTTTGATATTCTAGCTTACTTCCAAACTAATTCTATTGCTGAGACTAATCTT  
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTATTAAACATAACCTAAGAAG  
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF  
AAWCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTEFIVSDSTYSVASPYSTIPAPTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAALKNEAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATCGGTGCCCGGACTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTTCCTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTCCGCTTGGATATTGCATGGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCTG  
AGGAGAATGTGATCCGAGAATTAACTAAATGAGCTATAACCAGCGGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA  
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGCTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTCCCTCCAAGCTTGGTCAGTGTGTTACTGCTTATC  
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTAG  
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAACGTAAGATGCTGGGTATAGAA  
CGCTAACGAATTTCCCCAACGGACTCTGCTCCTAACGCCCTCTGGCTTCGTTATGGTC  
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAACGGAGAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTTGTGGGGATTGAGAACGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTGGAGGAGAACCTGGACTTCAC  
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCTGGGGACGTTGCCCTG  
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAAACGGCTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCGAGGGAGACCTGTTACCTACCAAGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGGCCCCAGAGAACGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT  
TTGGGACTACCAAGGCCCGTGCACCTGCGGAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGGCTGGAGCTGCGGGGTGTGGTCTTCCTTACAGTCCCCA  
ACGGCGCTACCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG  
GTGGCCTCTTGAGCAGCTCTCCGGCCTGGGAGGAGGGCTGGACTGGTCAACGCCGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGG  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTAGAACGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC  
AGCTTTGCCGCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCTGTGGTTACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGG  
CCGAAGCTTGGCTTCCCCGACCCGCAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGCCCTCCCTGCCGATTCCCTCACTGGCTGTGTTACTGAGTGGTT  
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT  
TTAAACATTTTTACTATTGGTAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGCCATTGCGGTTTGCGGCTCTG  
GAGGGTCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCAGAGTGGC  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC  
CAGCCTGGGGAAGAACGGCCTGGGGCTCCGGAGCTGGCTTGGCCTCTCCTGCC  
CACCTCTACTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAAACTCCCTCCCCGTT  
TCCCTCTCGGTTCAAAGAACGTTGTCATTGTTCTCCTGTTCCCTGTGTT  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR  
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAACGCTGGATAACAGGGGACCGGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCAGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGGACCGCATGGACCGCGCGGGGAC  
GGCAGGGCTGGGTGTCGCTGGCGAGCTTCGCGGTGGATCGCGCACACGCAGCAGCGCA  
CATACGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGCGTGG  
GTTGGGAGGAGCTGCGAACGCCACCTATGCCACTACGCGCCCGTGAAGAATTGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGCGTTCCGGTGG  
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCGAGG  
AGTTCCCTCACATGCGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGCCAGGTGGAGGAGTACATCGCGATCTGACTCAGCCGAGCCTGGGAGGA  
GGAGCCGGCGTGGTGCAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGGAGGACTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAAATGACCGGAGGAGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC  
TGTCCCTGTACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACACATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTCCCTGCCTGGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGACCTTGAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLRLHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGGCGGGCGCGGGTGGCAGGGATCCCTGACGCTCTGTCCTGTTCTTGTGCTCCAG  
CCTGTCGTCGTCGTTGGCCCCCGCTCCCCGCGGTGCGGGGTTGCACACCGATCCTG  
GGCTCGCTCGATTTGCCGCCAGGCGCCTCCAGACCTAGAGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTGTCCTCTCCTCTGCGCCGCCGGGATCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACGCGGGGCCTCCGCACCCCTGCCCTGCCATTCTCCCTCTCCCAG  
GTGTGAGCAGCCTATCAGTCAACCATGTCCGCAGCCTGGATCCGGCTCTGCCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGGCCGCAGCGAGGGAGCCGCTCCATTGCTATCACATG  
TTTACCAAGGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCCCTCAGTAGATGCCATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTCACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGTAAACGACTAAAGAAAACACCCGAGAAGAAAACGG  
CAATAAAGATTGTAAGCAGACATTGCATTTGATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAAATTACAGAAGAATTGGTGGAAAAGTGGCTCTAATGTTGGAAATTGGAACA  
GAAGGACCACATGTGGGCCCTGTTCAAGCCAGTGAACATCCAAAATAGAATTAACTTGAA  
AAACTTACATCAGCCAAAGATGTTTGTGCAATAAGGAAGTAGGTTTCAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT  
CGGAATAATGGCTTCTTCTTACACATGCCCAACTGGTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTAACT  
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCTC  
ATGCTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTCCAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCAGTTCACTGACTATAGCACCA  
AAGAGAAATGTCCTAGCTGTCACTGAAACATCCGTATATGAGTGGTGGAAACAGCTACTGGT  
GATGCCATTCTTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTCTGTTGGTGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAACATTGACAACAGAAAGAAAAGTACAAGGGATCCAGTGTGAAATTGTATT  
CTCATAACTGAAATGCTTCTGATCAGTACAGATACAAACTATTAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCAATCATGGCTTCTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLPGPAGSEAAPIAITCFTRGLDIRKEKADVLCPGGCLEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCC  
GGCGGCCTCCCGCGGGAGCGAGCAGATCCAGTCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCACCCCTGCTGTGCCCTGC  
TGCTGGCGGGCGGCGTCCCCACGGCCCCCGCCTCCGACGGGACCTCGGCTCAGTC  
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG  
GGTTGAGGAACGATGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCCAGCTAT  
CACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTCATCATCGACGAGGACTGTGGGCCAGC  
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT  
CTGCACCCGGACAGTGAGTGCTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGCAGCAATGGGACCATCTGTGACAACCAACAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCCTCCAGAGAGGCCGCTGTTCCCTGTGTGACACCCCTGCCGTGGAGGGCGA  
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTGGCAGCTTCATGGAGGAGGTGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGCCGCGCT  
GCACTGCTGGAGGGGAAGAGATTTAGATCTGGACCAAGGCTGTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA  
TCTTCTCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGTCTGGAGAGTCAGGAGGGTAAAC  
TGCAGGAGCAGTTGCCACCCCTGCCAGATTATTGGCTGCTTGCCCTCACAGTTGGCAG  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCCTGCTTGCAAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATTCC  
AGCAGTGTGCTCAGCTCCTACCTCTGCCAGGGCAGCATTTCATATCCAAGATCAATT  
CCTCTCAGCACAGCCTGGGGAGGGGTCTTGTCTCCCTCGCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTCAT  
CTGGTTGTGACTCTAACGCTCAGTGCCTCTCCACTACCCACACCAGCCTGGTGCCACCAA  
AAGTGTCCCCAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAATTAAAG  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
AGTGTGGGGCAGCGTCTTCTAATGAAGACAATGATATTGACACTGCTCCCTTTGGCAGT  
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA  
GTACTTAGTAATTGTAGGGCAGGATTATAAATGAAATTGCAAATCAGTGTGAAACATGGTT  
TGAAGACAATTATCAACCACGTGGAGAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTCCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA  
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCAATTAGAAATCAAGC  
ATAAAACTCAACTGCAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKVGNNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG  
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 85**

AAGGGAGGCTGGGAGGAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGAACCTG  
AAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCTCCAAACACACATGTGCATGTACACACACACATACA  
CACACATACACCTCCTCTCCACTGAAGACTCACAGTCACTCACTGTGAGCAGGTATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCCTGGCATTACCTCTGCAGCTCCTTGGCTGTTGAGTCAAAAAACATGGGAGGG  
CCAGGCACGGTGACTCACACCTGTAATCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTGAGGTCAAGGAG  
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTACTAAAAATACAAAATTAGCCAGGAGTGGTGGC  
AGGTGCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGATCGTGAATCCAGGAGGCGAGGATGCAGT  
CAGCTGAGTGCACCGCTGACTCCAGCCTGGGTGACAGAATGAGACTCTGTCACAAACAAACACGGGAGGA  
GGGGTAGATACTGCTCTCTGCAACCTCCTTAACCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGAACGCCCG  
GTGTTAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTGCTGACACCTTACCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCCTGCCCTGCAGCTCCACCATGAGGCTCTCGTGGCCCC  
ACTCTGCTAGCTTGGGTGGCTGGTGCACACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCCCTCTCA  
GTGTCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTACCGCGAGGCTACCAACTGTGGACTGCAATGA  
CCTATTCCCTGACGGCAGTCCCCCCGGCACTCCCCCGGCCACAGACCCCTGCTCCCTGCAGAGCAACAGCATTGT  
CCGTGTCGACCAGAGCTGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCTCCAGAACAGCTTTCGGA  
TGGCCGAGACTGTGATTTCAGCCCCCTGCCCCAGCTGCTGAGGCTGCACCTAGAGGAGAACAGCTGACCCGGCT  
GGAGGACACAGCTTGCAGGGCTGGCAGGCCACAGGAACCTATCTCAACCAACCCAGCTTACCGCATCGC  
CCCCAGGGCTTTCTGGCCTCAGCAACTTGCTGCCGTGCACCTCAACTCAACCTCTGAGGGCATTGACAG  
CCGCTGGTTGAAATGCTGCCCAACTTGGAGATACTCATGATTGGCGCAACAAGGTAGATGCCATCTGGACAT  
GAACCTCCGGCCCCCTGGCAACCTGCGTAGCCTGGCTAGCAGGCACTGAAACCTGCGGGAGATCTCGACTATGC  
CTGGAGGGCTGCAAAGCCTGGAGAGCCTCTTATGACAACCAAGCTGGCCGGGTGCCCCAGCGGGCACT  
GGAACAGGTGCCGGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCCAGGGTAGGGCCGGGGACTTGC  
CAACATGCTGCACCTTAAGGAGCTGGACTGAACACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT  
GAACCTCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCCTTATCCACCCCCGGCCCTTCCA  
CCACCTGCCAGATGGAGACCCCTCATGCTCAACAAACAACGCTCTCAGTGCCTTGACCCAGCAGACGGTGAGTC  
CCTGCCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCATCCGCTGGCCAATGC  
CACGGGACCCGTGTCGCTTATCGAGCCGCAATCCACCCCTGTGCGGGAGCCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGGACACTGTTGCCCTCATCTCCCCAGAAGCTTCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCATTGCCGGCACTGGCGAACCGAGATCTACTG  
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAGGAGGTACCGGGTGTACCCCGAGGGACCC  
GGAGCTGGAGGGTACAGCAGAAGAGGAGGGCTATACACTGTGTGCCAGAACCTGGTGGGGCTGACAC  
TAAGACGGTTAGTGTGGTGTGGCGTGCCTCTCCAGCAGGAGGAAGGACAGGGGCTGGAGCTCCG  
GGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGTCAACCAACACAGCTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCCGCTGCTCGGGGAACCCACAGCTA  
CAACATTACCGCCCTCTCAGGCCACGGAGTACTGGGCTGCCAGAGGCCTTACGAGCCTTAGGGGATGTCCTGGGCTCAT  
GTCCTCTGGCTCTCGCTGCCCTCTGGCAGCTGGCTAGGGCCACCTGGCACAGGGACAGCTTACGAGGAA  
GGGTGTTGGGGAGGGAGGGGGCTCTCCAGCCTGGCTTCTGGGCTGGAGTGCCTTACCTGTCCTGGGTTGT  
GTCTGCTCCCCCTCGCTGCCCTGGAAATCAGGGAGGAAGCTGCCAGATCTCAGAGAATCACTAGGACTACTTTTACCAA  
ACCATTGTCTCAAAATTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAATCACTAGGACTACTTTTACCAA  
AGAGAAGGAGTCTGGGCCAGATGCCAGGAAAGGGACATGGACCCACGTGCTGAGGCTGGCAGCTGGC  
CAAGACAGATGGGCTTGTGGCCCTGGGGTGCTTCTGCAGCCTGAAAAGTGGCCCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGGCCCTCTGCCCTCCCATCTT  
CTCTCTGCCCAGAGGCTCTGGCCTGGCTGTCCCCCTACCTGTGTCCTGGCTGCCAGACCCCTTCCCTTCTC  
TCTTCTCTGTACAGTCTCAGTTGCTTGTGCTCTGGCTGCCAGGGCTGAAGGGAGGCCACTCCATCTC  
CTCGGGGGCTGCCCTCAATGTGGAGTGCACCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGA  
CGCCTCATCTCAGCAGGCCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGAATTGTACCTTGTGGAGAA  
ATGTGTACACCTCCCCAACCGATTCACTCTTCTCTGTTGAAAAAATAAAAATAATAACAATAAAA  
AAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQILLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMDNFRPLANLRSVLVAGMNLREISDYALEGLQSLSESLSFYDNQ  
LARVPRRALEQVPGLKFLLDNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADTKTVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLAHLGTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGCCAAGGGCTGTTGACAAGGTGAAGAAGTCCGACCCATGTGGAGGAGGGGACATTGTGACCGCCT  
CTACATGCGGAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGGCCATCGACGGCTACCGCACCTACCGCTGTGCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCTCCTTCTACATCAGCTAGTCATCTTACGGCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTGGATCCGTGAGGAGGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCTTCTGAGTGGAGGAGTGGAGGAGTGGAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTGACTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCGACGTGACCATCCGCC  
CAGCATTGCCAGCTCACGGCCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGGCCGTGCGCT  
GGCCTTCTGCCGAGAACCTGCGGGCGCTGCACATCAAGTTACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGGGAGAACAAACGCTACATCGTCATCGA  
CGGGCTGCCGGAGCTAAACGCCCTCAAGGTGCTGCCGTCAAGAGCAACCTAACGCAAGCTGCCACAGTGGTCAC  
AGATGTGGCGTGCACCTGCAGAACGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA  
GAAGATGGCAACCTGACTGAGCTGGAGCTGATCCGCTGCCACCTGGAGCGATCCCCACTCCATCTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGAACCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCCTCACCTGCCCTAACGCTTCAAGCTGTGGTACAACCACATGCCCTACATCCCCATCCAGATGGCAACCTCACCA  
CCTGGAGCGCCTTACCTGAACCGAACAGATCGAGAACGACTCCCTCCGGAGCTTCCAGTGGCGGAAGCTGCGGGCCCTGACCT  
CTACCTGGACCTCAGCCACACAAACCTGACCTTCTCCCTGCCACATCGCCTCTGCGAGAACCTCCAGAACCT  
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGGCGGAAGCTGCGGGCTGCGACCT  
GGGCAACAACTGCTGCGACTGCGCTCCAGGGTGGCGAGCTGACCAACCTGACGCGAGATCGAGCTGCGGG  
CAACCGGCTGGAGTGCCTGCCGTGGAGCTGGCGAGTGCCTCAAGCGCAGCGGCTGGTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCAG  
GCCGGCCACAGCACCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCAGGGCAGGGCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCCTCGGGCTGGCAGGGCTGGCGCTTGTGAGTCAGGCCAGAGCAG  
GGACAGTATCTGGGGCTGGGCTGGGCTTCTCCCTCTGAGACTCACGTCCCCAACGGCAAGTGTGTTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTGCCACCTCCTCATCC  
CTGCCACCAGAGGTCTGGGACCCCTCACTTGTGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTCAGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTTCCCC  
TTGTCTTATTAGCGATGCCGCCGGCATTAACACCCACCTGGACTCAGCAGAGTGGTCCGGGCGAACAG  
CCATGGGACGGTCACCCAGCTGGCGCTGGCTCTGGCTGCCACGGGAGAGCAGGCCCTCAGCTGG  
AAGGCCAGGCCCTGGAGCTTGCTCTCAGTTGTGGCAGTTTAGTTTTGTGTTTTTTTTAATCAAA  
AAACAATTTTTAAAAAAAGCTTGAAATGGATGGTTGGGTATTAAAAAGAAAAAAACTAAAAAA  
AAAAGACACTAACGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT  
TGAACGTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTT  
CTATTGTTCTGGGAGGGAGGTTTTGTGTTGGTTGGGTTGGTGTCTGTTCTTCTCCTCC  
ATGTGCTTGGCAGGCACTCATTTCTGTTGGCTGCGGCCAGGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGTCCATTGCCACCTCCCTCCTGTCCTGCCCTGCCCTCTCCA  
CGCACAGTGTAAAGGAGCCAAGAGGGAGCCACTTCGCCAGACTTGTGTTCCCCACCTCTGCCATGGGTGT  
CCAGTGCCACCGCTGCCCTCCGCTGCTTCCATCAGCCCTGTCGCCACCTGGCTCTCATGAAAGAGCAGACACTTA  
GAGGCTGGTGGGAATGGGGAGGTGCCCCCTGGGAGGGCAGGCAGGGCTGGTCCAGGCCGGTCCCGTCCGGC  
CTGGAGTGCACACAGCCAGTCGGCACCTGGTGGCTGGAGGCCAACCTGCTTAGATCACTCGGTCCCCACCTT  
AGAAGGGTCCCCCCTTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTCTGTCTTAATGATTATGT  
CCATCCGTCTGTCGTCCTTGTGTTCTGCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAAA

## **FIGURE 88**

MRQTIIKVIKFILIIICYTVYYVHNIFKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQLNNNEWTLRQRLTKNAQDKLELHLFMLSGIPDVTVDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEIIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPQFYCRKRLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCCGTGGTACTTGTCATGGGAGCTGGCACTGCCGCTCTCCGT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGGCCTAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCGGGGGT  
TGCCTTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCCTGGGACCTTACCTGT  
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGGCCACCTAGTTGTCTTGTAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGCCCATCAGAAAGAA  
GCTCAAATTATTCTGAGGATCAATCTGGGAGGCCAGGCTACCAACGTCTTGTAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGGTAGGAGGCCTG  
GGTGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAAGCTAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCATTCTCCCTGTATCT  
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAAATTATTCTGCTTAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

**N-myristylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAAGGAGGCGGCCGTTATCAGGACCATGCAGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGAGCAGCCAACTCGGGCGTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTGAAACCTATACTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCAGTGCATCTCCCCACACCCCTCCAGGAAGTTCAAGGTGCCATCATAAACAA  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGCGGAAGGATGCCTGCTCGGTGACTCAGGTGGACCCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCVSLLSHRWALTAACFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSVGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCACACGCGTCCGGACCGGTGGAAAGGGCAGAATGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGGATCCCAG  
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGGCCATTCT  
CACTGACCCCTCCACACGGTGCAAAATGGCTCTGGCAGCCGGAGCCAGAAGTGCCATTCT  
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGCTGAGTTCATCACTATGTGGGAGGACCTACGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAACTTGACCTACAAGACGTGG  
GCTCTGGCACCAAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTCATGCCCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT  
ACCTGATGAGTGCTGGTCCAACATCTCACCTGGGTCTACAGTAGCCCTGCCGGCATGAG  
GGACAGGAGCCCTTCCTGCACTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCCCTGCTCTCGCTCAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTGGAAAGACACCAGTTCCGCCCTACCTTCCTGCCCTCAG  
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA  
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTCCTGAGCTCTAGCCCCCACCTGCCACCATTCCAGTTACTTCATG  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCCATCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGGATCCTA  
TCCTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTTTGGCTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCTGTAACAGGC  
TGGGAACACCAACTTCCAGCTTGTGAGACTCTACTCAACCCCTGACCCCTTCATC  
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTGACTCCAAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGCTTCAAAAGGGTTGTATAACAGACTCTGTGCACTA  
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT  
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGCTTATG  
GCCTTCCATCATAGTGCCCACCCCTCTCCTACTTAGCTTCCAGGTCTTAACCTCTCTG  
ACTACTCTTGCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTGC  
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCTGGAAACAAATCACTGACA  
TCTACAACCATTACCATCTCACAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIROAELLLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GGCGCGCGCTCTCTCCGGGCCACACCTGTCTGAGCGCGCAGCGAGCCGGCCGGCG  
GGGCTGCTCGCGCGGAACAGTGCTCGG**CATGG**CAGGGATTCCAGGGCTCCTCTCCTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTG  
GCCTGCATACCGCCTCCCTGTCGTCTTCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTATAAGGAACT  
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTATGCCAATGG  
CAGCCGACAGAGACGCCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAAGCATGTCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTCCTAAAGCCC  
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA  
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGGCAGAATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCCTACCAAGCAATGCGATGCCAGCCAGGGCCAGCGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG  
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
**TGAC**ACAGTGGTCCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTAGGAGAGGCC  
AAATTGTTTTTGTCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG  
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTG  
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAA

## FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD  
SGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL  
TAAHCIHDGKTYVK  
TQKLRVGFLKPKFDGGRGANDSTS  
AMPEQMFKQWIRVKRTHVPKGWIKGNANDIGMDYD  
AQP  
GASGSGVYV  
RMWKRQQQKWERK  
IIGIFSGHQW  
VDMNGSPQDFNV  
AVRITPLKYA  
QICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCC**ATGGTGGTT**  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCCTGGTGGAGC  
CCCACCCCTGTGTATTCCCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCCGCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCCATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGAACAGGCC  
GGGGTCTACATCAGCCTCTTGCGCACCGCTCCTGGTGGAGAACGATCGTCAAGGGTGCA  
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG  
CCGCGCGCTCT**TAGGGCGCAGCGGACCGGGCTGGATCTGAAAGGCGGCCAGATCCACA**  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGCGAAAGGAAACCCCTCCCCGACCCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAAC  
GACTCCGGCCCCGCCGGAGCGCTTTGTGTATATAATGTTAATTATTATT  
AGGTATTTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATT  
CTCCAAAAAAA

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT  
GGAGCTGCACAACCTTACCGGGCCAGGTATCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGAGAATCTGTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAAGGTGGTATGGCCAAGACAGAGAGGATC  
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC  
CGTGCCTCCAAATGTCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGAAGC  
CCGGAAGATGCTCAGGATTGCCCTACCTGGTAAGTGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCAGCAACGGGATTCCGGCTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCC  
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTA  
AACTGAGGTCCCTCAGGAGGCCAGAGAACTCTCTGGACCCCCAAGATGTCCCTGACAGGGCAAG  
GGAACTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTCAGTG  
AGGTCTTGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTCTGCCAGGTGCAAGGGCCCTGACA  
AGCCTAGCGTTGTCAGGGCTGAACCTGGCCCTGGTCACTGTGAGGGCCCTCTGG  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCAACTCAAAGGG  
TGAAGAGGTCACTGTCCTCTGTCACTCTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAAGGAAAGGCTACGGGCATGTGCCTCATCACACC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTT  
TTTGAATGGGGAGGCAGGGACGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCPSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHLPSLDEEPVTFPKSTHVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVVSGLNSGPVHVGPLLGLLLLPPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAAGTCAGGCTTTCATTGGAGCCCCCTAACAGAATCGGTCACTCTCCAAGTTATGGTGGACGT  
ACTTCTGTTCTCCCTGCTTTCACATTAGCAGACGGACTTAAGTCACAACAGATTATCTTCAT  
CAAGGCAAGTCATGAGCACCTTCAAAGCCTCGAGAAGTGAACAAACATGAATGGAGACCATTC  
AAATCTGGGACCAGTCTCGCAAATATTACACTCTCTGGCTGGAAACAGGATTGGAAACTCCCTGA  
ACATCTGAAAGAGTTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAAATATTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATGGAACCTGGTATTTGACAA  
TTTGGCCAACACACTCCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTAAACT  
GCCCAACTGCACATCTCGAACATGAAACGAAACAGATTAAAGTGTAGATGGACTGACATTCAAGGGCTTGG  
TGCTCTGAAAGTCATGAAATGCAAAGAAATTGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA  
CATGGAATTTTGAGCAGGACCTAACACACTAACAGAGATTACCAAAGGCTGGCTTACGGCTGCTGATGCT  
GCAGGAACCTTCATCTCAGCAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAACGCTCAG  
TGAGCTGGACCTAACATTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAACGTTACTAAATAC  
ACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT  
GGATCTGAAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGGGCTGACAAACTGAG  
GCGACTGATACTCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT  
GCATTAAATACATCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAACAACCT  
TCAGAGCTTGTAATGCCAGTTGTGCCATCCTCAGCTGCTAAAGGAAGCATTGGTGTAGCCAGA  
TGGCTTGTGTGATGATTCCAAACCCCAGATCACGTTAGCCAGAAACACAGTCGGCAATAAGGTT  
CAATTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGTGATTCCCAATGACTTTGCTTGGAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGAAATTATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCAC  
CATCCTCGGCTGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCATTGGTT  
ATCCTACTCTGCTAAAGCAAGCTTACAGTAAATATGCTTCCCTATTCAACCAAGACCCCCATGGATCTCACC  
CCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGTGGCACCAGCCCCCAGATAGCCTGGCAGAAGGA  
TGGGGCACAGACTTCCAGCTGCACGGGAGACGCATGTCATGTGATGCCCGAGGATGACGTGTTCTTATCGT  
GGATGTGAAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAACTTTCA  
AACTCTGACTGTCCTAGAAACACCATATTGGCGGCCACTGTGGACCGAACTGTAACCAAGGGAGAACAGC  
CGTCCCTACAGTCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACAAAGATGATAGCCCATTGGTGGT  
AACCGAGAGGCCATTGGTGCAGCAGCAACTCAGCTGATTATGTGGACTCAGATGTCAGTGTGATGCTGGAA  
ATACACATGTGAGATGCTAACACCTTGGCACTGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCAAC  
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTAGACGATGACGGATGGCCACTGTGGGTGTCGTGATCATGC  
CGTGGTTGCTGTGGTGGCACGTCACTCGTGTGGTGGTCATCATATACCACACAAGGGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTGTGTCATCTCAGGGACGTT  
AGCTGACAGGAGGATGGGTACGTGCTTCAGAAAGTGGAGCCACCAAGTTGTCACATCTTCAGGTGCTGG  
ATTTTCTTACCAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAAGCTGC  
CACAGATCTGTTCTTGTCCGTTTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGA  
TCCTTTGAAACATATCATACAGGTTGCACTGCCAGCAAGAACAGTTAATGGACCACTATGAGCCAGTT  
CATAAAGAAAAAGGAGTGTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATAC  
GTGGCCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAATGAAGGACCTGGAAATGAAAAACTGTG  
TCTAAACAAGTCCTTTAGATTAGTGCACATCCAGGCCAGCGTGGCTCGAGTAATTCTTCATGGG  
TACCTTGAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC  
AAGGCCCTTTATTGAAAGCTCATTCTCCCCAGACTTGGACTCTGGGTGAGACAGGAAAGATGGGAAAGAACAG  
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCAGGACTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACACATACACTCAAGTGAACCTTATT  
AAAGAGAGAGAACTTATGTTAAATGGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGAT  
GAACCAAAATTACAAAAAGTTATGAAATTTTACTGGGAATGATGTCATATAAGAATACCTTTAAACTA  
TTTTTTAACTTTGTTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATT  
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGTACCAATT  
TTAAATAGAAGTTACTCATTATATTGACATTATTTAATAAAATGTGCAATTGAA

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSAN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SA IPPKMFKLPQLQHLELNRRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEIQLQDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHLRSRLDDSSFLGLSLLNTHIGNNRVSYIADCAFRLSSLKTLDDLKNNE  
ISWTIEDMNGAFSGLDKLRRRILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLOQNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPOWVAENNFSFVNASCAPOLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPKNWTKDDSPVVTER  
HFFAAGNQLLIVDSDVSAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLLDDG  
WATGVVIIAVVCCVVGTSLVVVIIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTLAD  
RQDGYSSESSESHQFTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCSPDPRTVLMHYEPSYIKKKECYPCHPSEESCRSFNISW  
PSHVRKLLNTSYSHNEPGMKNLCLNKSLLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLNYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 103

GGGGAGAGGAATTGACCATGTAAGAGACTTTTTGGTGGTGGCTGTTGGGTGCCCTGCAAAATG  
AAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGATAAAACTGATTGCAAGAGAGAACGAAAC  
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTCACACAGGGAGCATTCAAGAATGAAA  
TAAACAGAGTTAGACCCGGGGGGTGGTGTGTTCTGACATAAAATAATCTAACAGCTGTTCCCTCC  
CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAGAAAAAAAGTATGTCATTTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTGGAAATGAAAGTTGGGCTTTTAGTAAAGTAAGAACT  
GGTGTGGTGGTGTGTTCTTCTTTGAATTCCCACAAGAGGAGAGGAATTAAATAACATCTGCAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAACCGAGCACAGTTGGA  
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTTCATCAACCTCTTTTTAAAT  
TTTATTCTTTGGTATCAAGATCATGCGTTCTCTTGTCTTAACCACTGGATTTCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAAGGACCAACACCAGATAAAATTATGAATGTTGAAAGAT  
GACCTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCCCTGCTGTGGT  
GCTGGCTCTCAACTTCTGTGGTGGCTGGTGCAGACCTGCCCTCTGTGTGCTCCTGCAAGCAA  
CCAGTTCAAGGATGATTGTGTTCCGAAAAACCTGCGTGGATGGCATCTCCACCAACACACGGCT  
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCCTAAGCAGCTTGGAAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGCTTCATGGTCTGGCAACCTAACACTCTGGA  
ACTCTTGACAACTGCTTACTACCATCCGAATGGAGCTTGTATACTGTCTAAACTGAAGGAGCTGGTT  
GCGAACAAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAAATTCTTGTGCGCCACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCTTGAAGGTCTGTCCAATTGAGGTATTGAAACCTTGC  
CATGTCAACCTTGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTCTGGAAATCA  
TTTATCTGCCATAGGCCTGGCTTTCCAGGGTTGATGACACCTTCAAAACTGTGGATGATACTGCCCAGAT  
TCAAGTGATTGAAACGGAAATGCCCTTGAACACCTTCAGTCACTAGTGGAGATCAACTGGCACACAATAATCTAAC  
ATTACTGCCATGACCTCTTCACTCCCTTGCACTCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTG  
TAACTGTGACATACTGTTCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGTG  
TAACACTCCTCCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCACATGCTATGCTCCCGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCACATC  
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGCGTACAAAGTGCAGGATAGCTGT  
GTCAGTGTGGTACGTTAAATTCAAAATGTAACCTGTGCAAGATAACAGGCATGTACACATGTATGGTGGTAA  
TTCCGGTGGAAACTACTGCTTCAGCCACCTGAAATGTTACTGCAAGAACCAACTACTCCTTCTTACTTTTCA  
AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGATGAGGCACGGACACAGATAACAAATGTGGGCTCCACTCC  
AGTGGTCAGTGGAGACCAATGTGACCACCTCTCACACACAGAGCACAAGGTCGACAGAGAAAACCTT  
CACCATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCTGAGACTACCAAAATCATCAT  
TGGGTGTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTATTTCTACAAGATGAGGAAGCAGCACCA  
TCGGCAAAACCATCACGCCAACAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCATGCCTGCTATGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACACAGTTAACACAATAAAATTCAATACACAGTTCACTGATGAACTGGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAACAAACAAATCAAAAAAA  
GACAGTTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA  
AAAAGAAAAGAAATTATTATTAAAAATTCTATTGTGATCTAAAGCAGACAAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFNDNRLTTIIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLPHDLFTPPLHHLERIHLHHNPWNCNCIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSGTLNFTNVTQDTGMYTCMVSNSVGN  
TTASATLNVTAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS  
VHEPLLIRMN SKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTCCCTCCCTGCTGTTGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCAGCGACCGC  
GAGGGCGGGCGTGACCCCTCGGCTGGAAGTTGTGCCGGGCCCCGAGCGCGCAGGGCTGGAGCTTCGGTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCAGCGCAGCCCTCCGTGCGCGCGCCGGGGTTGGGCTGCTGCTG  
GCGGTGCTGGGGCGCGCTGGCGCTGGCGCTGGACAGCGCGGTGCGGGGAACCTGGACTGCAAGCGCTAGCGCT  
GAGCGCCCAGTGGCCACTACCTGCCGTGCCCTGGGACCTGCTGGACTGCAAGCGCTAGCGCT  
CCCGAGCCACTCCGTCCCTGGGTGCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGAAGTCC  
ATGAGCCACCTCAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCATTCAAATCTGGACCA  
GTCTGGCAAATATTACACTTCTCTCTGGCTGAAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCTTGAAACTTGGACCTAGCAGCAACAATATTTCAGAGCTCCAAACTGCATTCCAGCCCTACAG  
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAATTGGCCAACACA  
CTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACTGCCCAACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCAAGGCCCTGGTGTCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGCTTTGGGGCTGAGCAACATGAAATTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGCAGGAACCTCAT  
CTCAGCCAAATGCCATAACAGGATCAGCCCTGATGCCTGGAGTTCTGCCAGAAGCTAGTGAGCTGGACCTA  
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTCCTGGCTAAGCTTAACATACACTGCACATTGGG  
AAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCAAGTTAAAGACTTGGATCTGAAGAAC  
AATGAAATTTCCTGGACTATTGAAGACATGAATGGTGTCTCTGGCTTGACAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGCTTACAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATTGCAATTAAATACA  
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGGAAACAAACTTCAAGGCTTGT  
AATGCCAGTTGTGCCCATCTCAGCTCTAAAGGAAGAACGATTTTGTGTTAGGCTTACAGTGGCTTGT  
GATGATTTCCTAAACCCCAGATCACGGTTCAGGCCAGAAACACAGTGGCAATAAAAGGTTCAATTGAGTT  
ATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTGGAAAAAAAGACAATGAACACTGCA  
GCTGAAATGAAATTATGCACACCTCCGGGCCAAGGTGGCAGGTGATGGAGTATACCAACATCCTCGGCT  
CGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCATTGGTTCATCCTACTCTG  
AAAGCCAAGCTTACAGTAATATGCTCCCTATTCAACAGACCCCCATGGATCTCACCACCGAGCTGGGCC  
ATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGCCACAGAC  
TTCCAGCTGCACGGAGAGACGCATGATGTGATGCCAGGATGACGTGTTCTTATCGGGATGTGAAGATA  
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGCAACTCTGACTG  
CTAGAAACACCATCATTTCGCGGCACTGTTGACCGAAGTGTAAACCAAGGGAGAAACAGCCGCTCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACGGACAAAGATGATAGCCCATTGGTGGTAACCGAGAGGCAC  
TTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGCTGGAAATACACATGTG  
ATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCCACTCCAACCTGCACTCC  
CAGATGACGCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGGTTGCTGT  
GTGGTGGGACGTCACTCGTGTGGGGTCATCATATACACACACAAGGCGGAGGAATGAAGATTGCA  
AACACAGATGAGACCAACTGCCAGATATTCTCTAGTTATTGTCTCAGGGAAACGTTAGCTGACAGGCAG  
GATGGGTACGTCTTCAAGAAAGTGGAAAGGCCACCCAGTTGTCACATCTTCAGGTGCTGGATTTCCTTACCA  
CAACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGAAGCTGCCACAGATCTG  
CTTGTGCTTGTGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGATCCTTTGAAACA  
TATCATACAGGTTGCACTGACCCAGAAACAGTTTAATGGACCACTATGAGGCCAGTTACATAAAGAAAAAG  
GAGTGCACCCATGTTCTCATCCCTCAGAAGAAATCCTGCAGACGGAGCTCAGTAATATATCGTGGCCT  
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAAATGAAAATCTGTTCTAAACAGTCC  
TCTTCTAGATTTAGTGCACAAATCCAGGCCAGCGTGGCTCGAGTAATTCTTCTAGGGTACCTTGGAAA  
GCTCTCAGGAGACCTCACCTAGATGCTATTCAAGCTTGGACAGGCCATCAGATTGTGCA  
GAGCCAAGAGCCCTTAT  
TTGAAAGCTCATTCTCCCCAGACTGGACTCTGGGTGAGAGGAAAGGAAAGGACAGATTTCAGGAA  
GAAAATCACATTGTACCTTAAACAGACTTGTGAAAGGAAACAGCTTACAGGACTCCAAATTTCAGTCTTATGACT  
ACATAGACTGAATGAGACCAAGGAAAGCTTAACATACTACCTCAAGTGAACCTTATTAAAAGAGAGAGAAT  
CTTATGTTTTAAATGGAGTTATGAATTAAAAGGATAAAATGCTTATTATACAGATGAACCAAATTAC  
AAAAAGTTATGAAAATTTTATACGGGAATGATGCTCATATAAGAATACCTTTAAACTATTTTAACTTT  
TTTATGCAAAAAGTATCTACGTAATTATGATATAATCATGATTATTTATGATTGTTATAATGCCAGA  
TTTCTTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGTGACCAATTGTTAAATAGAAGTT  
ACTTCATTATATTGCACTTAAATAAAATGTGCAATTGAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDGGRGELQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMHLQLSREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFPALQLKYLNLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQQLGALKSLKMQR  
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDLKNNEIS  
WTIEDMNGAFSGLDKLRLILQGNRIRSIKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTERHF  
FAAGNQLLIVDSDVSDAGKYTCMSNTLTERGNVRLSVPPTCDSPQMTAPSLODDGWA  
TGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGTIADRQ  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKGNVYGSDFETYHTGCSPDPRTVLMHDYEPSYIKKKECYPCHSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFOEENHICTFKOTLENYRTPNFOSYLDLT

Signal sequence:

amino acids 1-27

### Transmembrane domain:

HANDBOOK OF  
amino acids 808-828

#### N-glycosylation site

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

#### Glycosaminoglycan attachment site

## Glycosaminoglycan and amino acids 886-890

### Casein kinase II phosphorylation site

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

### Tyrosine kinase phosphorylation site

## tyrosine kinase phosphatase amino acids 667-675

N-myristoylation site

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 833-839

Leucine zipper pattern

leucine zipper pattern: amino acids 58-88, 65-87

## FIGURE 107

CAAAACTTGGTCTCGGGAGAGCGCCCAGCTGACTTGAATGGAAGGAGCCCGAGGCCGGAGCGCAGCTGAGAC  
TGGGGAGCGCTTCGGCTGTGGGGCGCCGCTCGGCGCCGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGCGCCACTGGTGTGAACCGGGAGAGGCCCTGGTGGTCCCCTATCCCTCCTTATATA  
GAAACCTCCACACTGGAGGAGCAGGGCAGGGCAGGGCTCATGGTGAAGCAAGGAGGCCGCTGATCTCAG  
GCGCACAGCATTCCGAGTTACAGATTTACAGATACAAATGGAAGGCGAGGGCAGAACAGCCTGCCCTGGT  
TCCATCAGGCTGGCCAGCGCATCTGACTCGCACCCCTGCAGGCACCATGCCAGAGCCGGGTGCTGC  
TGCTCTGCTGCTGCGGCCACAGCTGCACCTGGGACCTGTGCTGCCGTGAGGGCCCCAGGATTTGCCGAA  
GTGGGGCCACAGCCTGAGCCCAGAGAACGAATTGCGGAGGGAGCCGGTGTGGTACTGAGCCCTGAGG  
AGCCCCGGCTGCCAGCGCGTCAGCTGCCCGAGACTGTGCTGTCCAGGAGGGCTGTTGACTGTG  
GCGGTATTGACCTGCGTGAAGTCCCAGGGACCTGCCAGCACACCAACCAACCTATCTCTGCAGAACAAACCAGC  
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAAACGCCCTGA  
CTTCCGAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCGCTTCTGCCAACGCCCTGATCAGTGTGGACTTGCTGCCAATCTCACCAAGATCT  
ATGGGCTCACCTTGGCCAAGCAAACCTGAGGTCTGTGTAACCTGCACAACAACAAAGCTGGCAGACGCCGGC  
TGCCGGACAACATGTTAACGGCTCCAGCAACGTCAGGTCCTCATCTGTCCAGCAACTTCTGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAAAGCTGGAGAAGATCCCCGGGGCCT  
TCAGCGAGCTGAGCAGCTGCGCAGACTACCTGCAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA  
CCTTCTGGAAGCTCTCAGGCTGGAGTACCTGGATCTGTCCAGCAACAAACCTGTCTGGTCCAGCTGGCTGC  
CGCGCAGCCTGGTGTGCTGCACCTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCATCC  
GCAGCCTGGAGTACCTGCTGCACAGCAACAGCTGCCAGGAGCAGGGCATCCACCCACTGCCCTCAGGGCC  
TCAAGGGTTGCACACGGTGCACCTGTACAACAAACGCGCTGGAGCGCTGCCAGTGGCTGCCCGTGC  
GCACCCCTCATGATCTGCACAACAGATCACAGGATTGGCGCGAAGACTTTGCAACCACTACTTCTGGAGG  
AGCTCAACCTCAGCTACAACCGCATCACCAGGCCACAGGTGCACCGCAGCCCTTCCGCAAGCTGCCCTGCTGC  
GCTCGCTGGACCTGTGCGGCCAACCGGGTGCACACCGTGCACCTGGGCTGCCATGGCTAGCTGCTGAGG  
TCAAGCGCAATGAGCTGGCTGCCAGGAGGGCGCTGGCGCATGGCTAGCTGCTGAGCTGTACCTCA  
CCAGCAACCGACTGCCAGGCCAGGCTGGGCCCCCTGGGCTGGGACCTCGCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGCTCCCCGAGTCACCTGAGTACCTGTACCTGCAGAACAAACA  
AGATTAGTGCCTGGCTGGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGAGGTCTGGACATTGAAGGCAACT  
TGGCTGTGGCTCCGTGGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGAGGTCTGGACATTGAAGGCAACT  
TAGAGTTGGTGAACATTCCAAGGACCGTGGCCCTGGGAAGGAAAGGAGGAGGAGGAAGGAGGAGGAGG  
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTCTGC  
AGCACACGCCCTGTGTGCTGAGCCCCCACTCTGCCGTGTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGGCGTGTCCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCCCTCAAACCAACACAGTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAAGGGCTGCCCTGGCACACACAGGCCACCA  
TTCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCAAAGCCTATGCCACAGACAGCTCTGCCAGGAGAATCAGCCATAGCAGCTGCCGTGTGCCCT  
GTCCATCTGTCCGTCTGGAGAAGACACAAGGTATCCATGCTGTGGCCAGGTGCCACCCCTCT  
GGAACTCACAAAAGCTGGCTTTATTCTCTCCATCCTATGGGACAGGAGCCTCAGGACTGCTGGCTGGCC  
TGGCCACCCCTGCTCTCCAGGTGCTGGCAGTCACCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACCTTCCAATGGCAAGGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCCTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGCCAGGGAGGAAGGAGGCCAGCTGCACCTAGGAGACACCTT  
GTTCTCAGGCCCTGTGGGGGAAGTTCCGGGTGCCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAAAT  
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCCACCCCTCT

## **FIGURE 108**

MEGEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENFAEEEPVLVLSPEEPGPAAVSCPDCACSQEGVVDCGGIDLREFPGDLP  
EHTNHLSLQNNQLEKITYPEELSRLHRLETLNLQNNRLTSRGLPEKAFEHLTNLYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLNHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVAGLPRSLVLLHLEKNAIRSVDANVTPIRSLEYLLLHSN  
QLREQGIHPLAFQQLKRLHTVHLYNNALERVPSGLPDRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSPOVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGCGCCGCAGCAGACCTGCTCCGGCGCGCCCTGCCGCTGTCCCTCCGGAGCGGCAG  
CAGTAGCCCGGGCGCGAGGGCTGGGGTTCTCGAGACTCTCAGAGGGCGCTCCCATCGCGCCACCAACCC  
CAACCTGTTCTCGCGCGCACTGCCTCGCCTGGCCAGGACCCGCTGCCAACATGGATTTCCTGGCGCTGGT  
GCTGGTATCCTCGCTTACCTGCAGGGCGCGAGTCGACGGAGGTGGCCAGGCAAATAGTGTATCGAT  
TGGCCTATGTCGTTATGGTGGAGGATTGACTGCTGCTGGGCTGGGCTCGCCAGTCTGGGAGACTGTCAGCC  
TGTGTGCAACACGATGCAAAACATGGTGAATGTATCGGGCAAACAAGTGCAAGTGTATCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGGCCCTGTAAGCACAGGTGATGAAACACTTA  
CGGCAGCTACAAGTGTACTGCTCAAGGATATATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACCTG  
CTCCATGGCAAACGTCAAGTGTGATGGTGTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCGGCCT  
GCACCTGGCTCTGATGGGAGGACCTGTAGATGTTGATGAATGTGTCAGGAAGAGCCTGCCCTAGATT  
TAGGCAATGTGTCAACACTTTGGGAGCTACATCTGCAAGTGTATCAAAGGCTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTCATGACATAGACGAATGCTCACTGGTCAGTATCAGTGCAAGCAGCTTGCTCGATGTTATAA  
CGTACGTGGGCTCTACAAGTGCAGAAATGTAAGAAGGATACCAGGGTGATGGACTGACTTGTGTGATATCCAAA  
AGTTATGATTGAAACCTTCAGGTCAAATTGTAACAAAGGAAATGGTACATTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTGATGGAAAGTACTTGGTGGCTCCGAAGACACCATAATTCTCTCTATCATTACCAA  
CAGGCCTACTTCTAACGCCAACACAAGACCTACACCAAGGCCAACACCAATTCTACTCCACCACCACCA  
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCGGACTGACAACATAGC  
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACGCCCTAGAAACCCAGG  
AGATGTGTTCACTGGTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACTGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAGCCCCAGG  
GGGAAAGCTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG  
GGGAAGAAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTGGCAGGGGCTGACATCAAGAGCGAATCACA  
AAGATGATTAAAGGGTTGGAAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGAAG  
AGAAGACTGGGGCAAACCATGGTCTTCAAGTATATGAAGGGTGGCACAGAGGGTGGGACAGCTG  
TTCTCCATATGCACTAAGAATAGAACAGGAAACTGGCTTAGACTAGATATAAGGGAGCATTTCTGGCAGG  
GCCATTGTTAGAATACTTCATAAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTTTCTAAAAAATTAGA  
AAAAAATTGTCATTAAAGATGGTTAAAGATGTTCTTACCAAGGAAAAGTAACAAATTATAGAATTCTCCAAA  
AGATTTTGTGATCCTACTAGTAGTATGCACTGGTAAAGGGAAAGGCCACAAATGCTGAGCTCACTGAAATA  
TCTCTCCCTATGGCAATCTAGCAGTATTAAGAAAAAGGAAACTATTTATTCCAATGAGAGTATGATGGAC  
AGATATTTAGTATCTCAGTAATGCTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC  
TTTCATTGTTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAACACAGTTAGAGAG  
ATTTTCATGGGTGCAATTCTCTGCTTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC  
ACACCGGCAGACCTTCCTCACCTCATCAGTATGATTGAGTTCTCTTATCAATTGGACTCTCCAGGGTCCAC  
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCAATTAACTGGTAAAGGCAGGGCTGG  
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTCAATT  
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAATTAACTTTACTTTGATGCCAA  
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTAAATGTTT  
CTAAAATAAAATGTTAGTGGTTTCCAAATGGCTAATAAAAACAATTATTTGTAATAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCV DVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPTT PERPTTGLTTIAPA A STPPGGITVDN  
RVQTDPQKPRGDVFSVLVHSCNFDHGLCGWI REKDNDLHWEPIRD PAGGQYLTVSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTOI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## **FIGURE 111**

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTTGCCCTTAGATTGTGA  
**AATGTGGCTCAAGGTCTTCACAAC**TTTCTTGCACAGGTGCTGCTCGGGGCTGA  
AGGTGACAGTGCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTCCACACTCCAGCAGACATCCAGATCATGGCTATTGAGAGACCCCA  
CACAAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGGTCTGACTTGGAAATACC  
AACACAAGTTACCATGATGCCACCAATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGGAAATGGAACCTATCTGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTCAGATTACCTCCCT  
CTGGGGCTGTGGAGTATGTGGGAAACATGACCTGACATGCCATGTGGAAGGGGGACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT  
GCCTGGTGAGGAACCTGTCAGTGAATGGAAAGTGTATCATATTGCCATCATATTATT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAACAGACAATGGACTATGTGTGCTGTGCTTACAACAAACATAAC  
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG  
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT  
ATATCCATGTGCTTCTCTTCTATGGAAAAAATATCAACCCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAACAGAACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTATCGGGCAAGATTGACAGTACAGT  
GTATGAAGTTATTGACATCCCTGCCAGCAGCAAGACCATTCCAGAGT**TGA**ACTTTCATGG  
GCTAAACAGTACATTGAGTGAATTCTGAAAGAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAACACCAGGACCAACACACTCTACTCATTATTCTTTACA  
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATAACAAATGTCTT  
GTGCAACAGAAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCCTCATAGTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTTCAGGAAATCTATCTGTTATTGACAA  
CAAAGTAATAAGGATGGTTGTCAACAAAACACTATGCCCTCTCTTTCAATCACC  
AGTAGTATTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTA  
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGCTTTAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNVKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDPCSADSHPPNTYSWIRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGCGAAATGGCGCCCTCCGGAGTCTGCAGTTCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGCTCCCTGGACGCACGGCGGGAGAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT  
TGTCAAAAATCTTCACCGGAATGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGTTATCATAACTGCTC  
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTTATAAGTGTAAAGAGTGGAGAGTATTGAGCCGTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCTTTGTCCTCAAAAGGCAGACACAGCCATACCCATACCCCTCAAAAAAAAT  
TATTATCAGAATCTGCACAACCTTGAAAGGAGGAGAACAGAGGGGATGAAGAA  
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC  
CATAAAGACAAACGCTCTGGGTCATCATTGCCACAGATAAATCCTAGTTAAATTATAG  
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAAATATTGCAAGGTTCACTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATAACAGTTGAAATATGATTAAGCACAGTATGATG  
GTTAAATAGTTCTCTAATTGAAAGGATTTGCAAGCAATAAGATTATGTATATTGT  
TTAATAATAACCTATTCAAGTCTGAGTTGAAATTTACATTCCCAAGTATTGCAATTAT  
TGAGGTATTTAAGAAGATTATTAGAGAAAATATTCTCATTGATATAATTCTCTG  
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTTAGTTCACTGACAATTCTGGTCTTTAGAGGTATTCAAATTTCTTGT  
ATTTTAGTTTATGCAACTAATAAAACTACCTTACATTAATTAAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAGTTCACTGTTATTCTCTGATT  
CAACAAAAGTTGATTCTCTGTATTCTTACTTACTATGGGTTACATTTTTATT  
CAAATTGGATGATAATTCTGGAAACATTTTATGTTTAGTAAACAGTATTGTTGTT  
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTGAATTAAAATT  
TTGCCACTTTTCAGATTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTT  
TTCTTTGGATGTGAAGGTGAACATTCTGATTGTTCTGATGTGAAAAGCCTGGTA  
TTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAG  
CATCTTCTTGATATGCTTAATGTATTGTCCTCATACAGAAAGTTCTTAATTGAT  
TTACAGTCTGTAATGCTGATGTTAAAATAACATTATTATATTGTTAAAGACAA  
ACTTCATATTATCCTGTTCTCCTGACTGGTAATATTGTTGAGGATTTCACAGGTA  
AAGTCAGTAGGATGGAACATTAGTGTATTCTACTCCTAAAGAGCTAGAATACATAGTTT  
CACCTTAAAGAAGGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTCTGTAATGTCCTCTTCTAGGCTCTGCTGTGAATCCATTAGATTACAG  
TATCGTAATATAACAGTTCTTAAAGCCCTCCTTAGAATTAAAATATTGTACCATT  
AAAGAGTTGGATGTGTAACTTGTGATGCCTAGAAAATATCCTAAGCACAAATAACCT  
TTCTAACCACTCATTAAAGCTGAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCP SKRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCGAGTGTCCAGCTGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTTGTAACCCAGTGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGCTGC  
ATTGCTGATGGCCTGGTTGGTGTCTGAGCTGTGTCAGGCCGAAATTCTTCACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTGTGAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATAACAGGCTGGACCCAGGCACAATTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGCTTCCAGTTGGTGTGACCTGACCCTGGAGCTCACCCGCCGCTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGATCTGCGGTACTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCCTGTGGACTACCTGCTGAGAGGGATTTACGAGAGCCTCTGCTGTGG  
GAGGGTGTCAAACGTACACCCCCTAGACAGAAGAGGCTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATGCCCTCAAAGAGGAGGACGAGTGGACAGCCCGACA  
TCGTCAGGTACTACGATGTCATGTCAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGACGAGCCACCGTCTGATCCAAAGACAGGAGTCCTCACTGCGCCAGCTA  
CCGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGAGAATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGGACCTTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGTAAAGCTG  
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACACCTCTTGCAGGGAGGGAAAGGTGACTACCGAACAGACATGCTGCC  
TGTGCTTGTGGCTGCAAGTGGGTCTCAAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTGTGACATCCTTCTGTCCTCCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTGGAGAAATGAATGTTGTCAGGAGCAGAGGGAGACCATACTAGGGCAGTCCTGT  
GTGACTGAAGTCCCAGCCCTTCATTGAGCTGACCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTTGTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCTACCAAGAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVILSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGEGLPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPHSERAGGNLR  
YFEQOLLEEREKTLTNQTEAELATPEGIYERPVDFPERDVYESLCRGEGVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIYRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKFHERGQEFLRPCGSTEVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGAAGACAGACATAATCCAGTGTGAGTGAATTGATTGT  
TTCATTTATTACCGTTTGGCTGGGGTTAGTCCGACACCTTCACAGTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTTGGGATGCTGGTCTGGAAGCCAGCGGCCCTGCTCTGTCTTGGCCTCATGACCC  
CAGGTTCTGGTAAACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCCACCTGGCAGGGCTACCAACCATTCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGCGCTTC  
CCCTCATCTAGGGCTGTCCTGGGGTGCAGCCTGAGCCTCTGCGGGTTTCTGGATCCAGGGGGAGGGAGAAG  
ATCCCTGTGTCAGGGCTGAGGGAGGGCCACAGAATCCAGATTGAGCTCGCTAGACCAAAAGTG  
ATGAAGACTTCAAACCCGGATTGTCCTTACTACAGGGACCCAAACAGCCCTAACAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGCTCCCGTGAGGGTTGCTGGTGGCTCTGACACTCCGAGCTACACTGTCCA  
CTTGGCCGTGGTGTGAACCGTACGGTGGCCATCACTCCCTCGTTACTCTACTTCACACTGGCAGGGGG  
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC  
GCCACCTTCACACACACTTGGGCCACTACGACTGGTCTTCATCATGCAGGATGACACATATGTGAGGCC  
CCCGCCTGGCAGCCCTTGCTGGCCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATG  
GCGCAGCGAGCAGGCCGGTACTGTCATGGGGCTTGGTACCTGTCACGGAGTCTCCTGCTCGTGC  
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGCCTCTGACGAGTGGCTGGACGCTGCCCTATTG  
ACTCTCTGGCGCTGGCTGTCTCACAGCACCAGGGCAGCAGTATCGCTCATTTGAACGGCAAAATAGGG  
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCGTGCACCCGTCTCCGAAGGTACCCCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTTGGAGTTGGAGCAGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA  
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGGTGGCTCCCTGCTCCTTCA  
CACCAACTCTGCTTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCTGTGCAGATGGGG  
CTCCCAAGTGCCACTACAGGGGGTAGCAGGGGGACGTGGGTATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGCGCTATCAGCCCCGCTCGCCTTCCAGAACGAGCAGCAGTGCACAGGCTATGGCGCTTCGACCAGCAC  
GGGGCATGGAGTACACCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGACCGGGCCCTGGCTCGCA  
GGGTAGCCCTGCGGCCACTGAGCCGGGTGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC  
AGCTGGTGTGCACTCCTGGCTGAAGCTGTCAGGCCGGCTTCCCTCGAGGGCTTGCAGCCAATGTCC  
TGGAGGCCAGAGAACATGCAATTGCTCACCCCTGTTGCTGTGACCGAGGCTACGGGCCACGAGAAGGTGGCGTGGAGCTCCAG  
ACCCATTCTGGGGTGAAGGCTGCAGCGGGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCTGGCTCG  
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGACCCCTGTGGACACTCTCT  
TCTTCCTTACCAACCGTGTGGACAAGGCCCTGGGCCGAAGTCTCAACCGCTGTCCATGAATGCCATCTGGCT  
GGCAGGCCCTTCTTCCAGTCCATTTCAGGAGTCAATCTGCCCTGTCAACACAGAGATCACCCCAAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCGGGGGGCTCTATAGGGGGAGATTG  
ACCGGCAGGCTCTGCGGAGGGCTGTTCTACAACGCTGACTACCTGGCGGCCGAGCCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGCTGGAGGGTGTGGATGTTTCTCCGGTCTCAGGGCTCC  
ACCTCTTCGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGGAGACTGCCAGCCACGGCTCACTGAAG  
AACTCTACCACCGCTGCCGCCTCAGCAACCTGGAGGGCTAGGGGGCGTGGCTATGGCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCGCTGGGGCCCTAACCTCATTACCTTCTTGTCTGCCCTCAGCC  
CCAGGAAGGGCAAGGAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA  
ACATGTCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD  
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDS LGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLLECVTQRGHRRALARRVSILLRPLSRVEILPMPYVTEATRVQLVPL  
VAEAAAAPAFLEAFAAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLRNRCRMNAISGWQAFFP  
VHFQEFPALSPQRSPGPPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVMDVFLRSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAGQLAMALFEQEQANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGCAGCGCTGCCTTCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG  
AAGCATTCTGTGCTTGTACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG  
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACAACG  
GTTCTCCTTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTGTTACTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGTGATGGGTATACGCCCTAGGGCATTTGGCATATTTCAAT  
GATGCATTGGTTTCTTACCTCAAATGGTCTGACAATGACTAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTTAGTAGTAACATACATACCAA  
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGTAATG  
TGTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAAACTATTAATAAAATATTAT  
GTGATAAAATTCTAAATTGAAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTGTGTTGTTACTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTTCTCAAAATGTACAACAAAGCAACTAAAGAAA  
ATTAAAGTGAAGTGAAGGAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

CCACACGCGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTTCTTCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTTCTCAGTGCCTGTTCATCACCAGATGTGTTGTGACATTCGCAT  
CTTCAAAACCTGTGATGAGAAAAAGTTCAGCTACCTGAGAATTCACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGCCATTGAACGGAAATATTTCAATCC  
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAACTGCTCAGC  
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTCTACAAGA  
AACCTAAAATGAGAGAGTTTTATTGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA  
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAAATTGGA  
ATGATGTAACCTGTTCCCTCAATTATTTCGGATTGTGAAATGGTAGGAATAAATCCTTG  
AACAAAGGAAAATCTCTTAAGAACAGAAGGCACAACCTCAAATGTGTAAGAAGGAAGAGCA  
AGAACATGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC  
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAA  
AA  
AAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS  
NPRQNWNVDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCCTCGGCTGCCTGACTCTTCCCTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGCTGTAATC  
TCAAATCCAGCAATCGAACCCAGTGTACAGGAATTGAAAGTGTGAACGTGCTTGCATATTACGGATTGCG  
AGACAAGTGAACCCAGGATCGAGTGAAGAAAATTCAAGATGAACAAACACATATGTGTTTTGACAACAAAA  
TTCAGGGAGACTTGGGGCTGCTGCAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTATCGCTGTGAGGTGCTGCTGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGAACCCCTGCTGTAGAGTGCCTGAAGGCTGTACAGTAGGCAAGATGGCAACACTGC  
ACTGCCCAGGAGAGTGAAGGGCCACCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT  
CCAGAGCCAATCCAGATTGCAATTCTTCTTCACTTAAACTCTGAAACAGGCACATTGGTGTACTGCTG  
TTCAAGGACGACTCTGGGAGACTACTGCTGCTTCCAACTGACCGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGGGAATTATTGGGGGTTCTGGTGTCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCACTTCAGACACAAGTCATCGTTG  
TGATCTGAGACCCCGCGGTGGGCTGAGAGCGCACAGAGCGCACGTGACACATACTCTGCTAGAAACTCCGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAGCTTTGCTTTGGCAAAGTTGACCA  
CTACTCTTCTACTCTAACAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATATAACCA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGCTCTAATCTGTTCTGGCTGATTCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTGCTCACGTAACGCCCCGTGCTGGGCTGTGAAGCCAGCATGTTACCAACTGGTCGTT  
CAGCAGGCCACGACAGCACCAGTGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGGGAAACCA  
GAAAAGGCTTCTACACAGCAGCCTTACTTCATCGGCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCAGTGTCCATTGTGAGAAGCTTTGGATCAGCATTGTAAGGAAACACAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTAGGATTAAAGGAA  
ACCTTCGTCTTAGGCTAAGTGTAAAGTGTACTGAAATATGCTTTCTATGGGTCTTGTATTAAAGGAA  
TACATCTAAATTGGCTAAGGATGTATTGGATTATTGAAAAGAAATTCTATTAAACTGAAATATAATTGT  
CATACATGTTAAATAACCTATTGGTAAAGGTTCAACTTAAGGTAGAAGTCAAGCTACTGTGTTAAAT  
TGGAAAATATCAATAATTAGAGTATTGGTACCGAAGGAATCTCTCATGGAAGTTACTGTGATGTTCTTCT  
CACACAGTTTACGCTTTTCAAGGGAACTCATACTGCTCACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAATTCAGGTTAAAGCAATGTTGAATCAGTTGCTCTTCAAAAGAACCTCTCAGGTTAGCTTGAAC  
GCCTCTTCTGAGATGACTAGGACAGCTGTAACAGGACAGGGCACCCAGAAGCCCTCAGATGTACACAGATG  
CCAGTCAGCTCTGGGGTTGGCCAGGGCCAGGGCCCCCTCTAGCTCACTGTTGCTCTGCTGCTGCCAGGAGGGCCT  
GCCATCTTGGGGCTGGCAGTGGCTGTGCCCCAGTGAGCTTACTCACGTGCCCTTGCTTCACTCAGCACAGC  
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCCAGCTTGGCTCCTGTAACAGACCTCT  
TTTGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGGTTTAAGTTGTTAAATTGGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCAAATCAAGTGTCAAGTACAATAACATTGGTAAAGGAAATGGAT  
CCCACGTGTTCTCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCGATTTCAAAACAAACATGAT  
GGAGTGGCGGCCAGTCCAGCCTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGGGAGGAAAG  
TGAAACGCCGAATCAAAAGCAGTTCTAATTGACTTAAATTGTCATCCGCCGGAGACACTGCTCCATT  
TGTGGGGGACATTAGCAACATCACTCAGAAGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA  
GAATGGCTCTCACTACTCACCTGTCTTCACTGCTTCAAGTGTCTGGGTTTTATACCTTGACAGCTTTTTT  
AATTGCTACATGAGACTGTGTTGACTTTTTAGTTATGAAACACTTGCCGCAGGCCCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGATGCCATCTGATGCTTACAGTCAGTT  
CCTCCATCATGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCACTGCTCCAGCCTCCT  
TCTTGGTTGTCAGTGTAGGGTAGGCTTATTGCCCTTCTTACCCCTAAACCTTACACTAGTGCCA  
TGGGAACCAAGGCTGAAAAGTAGAGAGAAAGTGAAGTAGAGCTGGGAAGTAGCTGCCATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTAAAGATATGAATGTGACTCAAGACTCGAGGGCAGACGAGGCTGTGATTCT  
GCCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC  
CTCATTTATAAAAGCTCAAAAAACCCA

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIA SNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRKSSFVI
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267